

DATE : 22.05.2023

Db 193 PLYLGGVQLEKGRDLRAEINRPNLYLDFAESGQVYFG 229

## RESULT 10

154490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C&gt;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

C:Accession: 154490

R:Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leucopus

A:Reference number: 154490; MUID:92218012

A:Accession: 154490

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 &lt;RES&gt;

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: PLTNF

A:Introns: 62/3; 81/1; 97/1

Superfamily: tumor necrosis factor

Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 7.9%; Score 132.5; DB 2; Length 235;  
Best Local Similarity 25.3%; Pred. No. 0.0011; Mismatches 54; Indels 43; Gaps 7;

Qy 163 OPFAHLTINATDIPSGSHKVSLSWYHDSRWAKISNMTFSNG-----KLIYNQDGFYLL 216

Db 90 KPAHVAVN-----HQVDEQLWLSRG-----ANALLANGMDKLNQVLPADGLYLIV 137

Qy 217 YANICFRHETSGDLATEYLQLMVYTK-----TSIKIPSSHTLMKGGSTYK 264

Db 138 YSOVLFK-----GQCSSYVLLTHVSRFAVSIEDKVNLSAISKPCPKETPEGSELKPW 192

Qy 265 SCNSEFHYISINVGGFFKLRSGEISIEVNSPLLD-PPDQATYFG 309

Db 193 -----YEPYILGGVQLEKGRDLRAEINRPNLYLDFAESGQVYFG 231

## RESULT 11

JU0029

tumor necrosis factor alpha precursor - rat

N:Alternate names: cachectin; TNF alpha

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 04-Feb-2000

C:Accession: JU0029; JN0868; S21674

Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.

Viric. Biol. Chem. 53, 1733-1736, 1989

A:Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor

A:Reference number: JU0029.

A:Accession: JU0029

A:Molecule type: DNA

A:Residues: 1-235 &lt;SHI&gt;

R:Kwon, J.; Chung, I.Y.; Benveniste, E.N.

Gene 132, 227-236, 1993

A:Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.

A:Reference number: JN0868; MUID:94040766

A:Accession: JN0868

A:Molecule type: DNA

A:Residues: 1-235 &lt;KWO&gt;

A:Cross-references: GB:L00981; NID:g205253; PIDN:AAA16275.1; PID:g205254

R:Exler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.

Biol. Chem. Hoppe-Seyler 373, 271-281, 1992

A:Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro

A:Reference number: S21674; MUID:92329007

A:Accession: S21674

A:Molecule type: mRNA

A:Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 &lt;EST&gt;

A:Cross-references: GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47146.1; PID:g395370

C:Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

F:80-235/Product: tumor necrosis factor #status predicted &lt;MAT&gt;

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted

F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:148-179/Disulfide bonds: #status predicted

Query Match 7.8%; Score 131.5; DB 2; Length 235;

Best Local Similarity 25.3%; Pred. No. 0.0013;

Matches 41; Conservative 27; Mismatches 59; Indels 35; Gaps 7;

Qy 163 OPFAHLTINATDIPSGSHKVSLSWYHDSRWAKISNMTFSNGKLIYNQDGFYLLYANI 220

Db 90 KPAHVAVN-----HQVDEQLWLSRG-----ANALLANGMDKLNQVLPADGLYLIVSQV 141

Qy 221 CFRHETSGDLATEYLQLMVYTK-----TSIKIPSSHTLMKGGSTYKWSGNS 268

Db 142 LFK-----GQCDDVLLTHVSRFAISYQKVSLSAISKPCPKDTEGAEALPW----- 192

Qy 269 EFHYISINVGGFFKLRSGEISIEVNSPLLD-PPDQATYFG 309

Db 193 ---YEPYILGGVQLEKGRDLRAEINRPNLYLDFATESGQVYFG 231

## RESULT 12

I49139

lymphotoxin-beta - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I49139; I49138; I49076

R:Lawton, P.; Nelson, J.; Fizard, R.; Browning, J.L.

J. Immunol. 154, 239-246, 1995

A:Title: Characterization of the mouse lymphotoxin-beta gene.

A:Reference number: I49138; MUID:95088371

A:Accession: I49139

A&gt;Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-306 &lt;RES&gt;

A:Cross-references: EMBL:U16985; NID:g577830; PIDN:AAA70089.1; PID:g577831

A:Accession: I49138

A&gt;Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-306 &lt;RES&gt;

A:Cross-references: EMBL:U16984; NID:g577431; PIDN:AB60493.1; PID:g577432

R:Pokholok, D.K.; Maroulakou, I.G.; Kuprash, D.V.; Alimzhanov, M.B.; Kozlov, S.V.; N.

Proc. Natl. Acad. Sci. U.S.A. 92, 674-678, 1995

A:Title: Cloning and expression analysis of the murine lymphotoxin beta gene.

A:Reference number: A55602; MUID:95148600

A:Accession: I49076

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-306 &lt;RE2&gt;

A:Cross-references: EMBL:U12029; NID:g515508; PIDN:AAA67716.1; PID:g515509

C:Genetics:

A:Gene: LT-beta

A:Introns: 54/3; 160/1

Query Match 7.7%; Score 130.5; DB 2; Length 306;

Best Local Similarity 22.1%; Pred. No. 0.0023;

Matches 55; Conservative 38; Mismatches 87; Indels 69; Gaps 12;

Qy 105 ESQDTKLIP--DSCRRKQAFQAGVQKELQHVQSHIRAEKAMVDGSGWLDLAKRSKLE 161

Db 86 ETPDRLHPQRSNAGRNLAISTSQGPV-----AQSREASAMMTI----- 124

Qy 162 AQPFAHLTIN--ATDIPSGSHKVSLS-----SWYHDSRWAKISNMTF----- 201

Db 125 LSPAADSTPDGVOQLPKGEPTDLNPELPAHLIGAMNSGGGLSWEASQEEAFILRSQAQ 184

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho  
F:1-77/Domain: propeptide #status predicted <<PRO>  
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
F:80/Binding site: myristate (Lys) (covalent) #status predicted  
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:146-178/Disulfide bonds: #status predicted

Query Match 8.1%; Score 137; DB 1; Length 234;  
Best Local Similarity 26.1%; Pred. No. 0.00046;  
Matches 52; Conservative 30; Mismatches 71; Indels 46; Gaps 10;

QY 134 IVGSHIRAEKAMVDGSG---LDLAKRSKLEA---OPFAHLTINATIPSGSHKVSLSGSW 187  
DB 55 VIGPQ---REQSPAGSFNRPVQVILRSSQASQNKPKVAHVAN-----ISAP 100  
QY 188 YHNRGWAKISNTMFSNG-----KLIVNODGYIYLYANTCFRRH-----TSGDL 231  
101 GOLRWGDSYANALMANGVELKDNQVLPDGLYISQVLFGRHGCPSTPLFTHTISRI 160  
QY 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYVSGNSEEHFYSINVGFFKLSGEEISI 291  
DB 161 AVSY-OTKVNIL-SAIKSPCHRETLEGAPKP-----YEPYOGGVFOLEKGRLSA 211  
QY 292 EVSNPSLLD-PQDATYFG 309  
DB 212 EINLPYLDYAESGGVYFG 230

RESULT 9  
OWHUN  
tumor necrosis factor alpha precursor [validated] - human  
N:Alternate names: cachectin; TNFA  
C:Species: Homo sapiens (man)  
C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 08-Dec-2000  
C:Accession: A93585; S36153; A4189; B61478; I53311; S62610; I54522; A01646; B23  
N:Wedin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D  
Nucleic Acids Res. 13, 6361-6373, 1985  
A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chr  
A:Reference number: A93585; MUID:86016093  
A:Accession: A93585  
A:Molecule type: DNA  
A:Residues: 1-233 <NED>  
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
R:Irish, F.J.M.; Bouguerel, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka  
Nature Genet. 3, 137-145, 1993  
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a  
Reference number: S36152; MUID:93272029  
A:Accession: S36153  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-233 <IRI>  
A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992  
R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.  
Nature 312, 724-729, 1984  
A:Title: Human tumour necrosis factor: precursor structure, expression and homology to  
A:Reference number: A93351; MUID:85086244  
A:Accession: A93351  
A:Molecule type: mRNA  
A:Residues: 1-233 <PEN>  
A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210  
A:Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyeloc  
R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;  
Science 228, 149-154, 1985  
A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.  
A:Reference number: A44189; MUID:85142190  
A:Accession: A44189  
A:Molecule type: mRNA  
A:Residues: 1-62, 'S', 64-233 <WAN>  
A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738  
R:Fukuda, S.; Ando, S.; Sanou, O.; Tani, M.; Masaki, N.; Nakamura, K.I.; Ad  
Lymphokine Res. 7, 175-185, 1988

A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta  
A:Reference number: A61478; MUID:88301617  
A:Accession: B61478  
A:Molecule type: protein  
A:Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174  
R:Mamenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawasaki  
Eur. J. Biochem. 152, 515-522, 1985  
A:Title: Molecular cloning and expression of human tumor necrosis factor and compari  
A:Reference number: I53311; MUID:86030296  
A:Accession: I53311  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-233 <MAR>  
A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764  
A:Experimental source: U-937 cells; Yamamoto, S.; Fukuda, S.; Kurimoto, M.  
R:Takura-Yamamoto, R.; Yamamoto, S.; 431-437, 1996  
Eur. J. Biochem. 235, 431-437, 1996  
A:Title: O-Glycosylated species of natural human (tumor-necrosis factor-alpha.  
A:Reference number: S62610; MUID:96202967  
A:Accession: S62610  
A:Molecule type: protein  
A:Residues: 77-99 <TAK>  
R:D'Alfonso, S.; Richiardi, P.M.  
Immunogenetics 39, 150-154, 1994  
A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter  
A:Reference number: I54522; MUID:94102809  
A:Accession: I54522  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-8 <DAL>  
A:Cross-references: GB:S68530; NID:g544751  
R:Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.  
J. Exp. Med. 176, 1053-1062, 1992  
A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific  
A:Reference number: A59163; MUID:93018920  
A:Contents: annotation; identification of myristylated lysines  
R:Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Hensel, W.J.; B  
J. Biol. Chem. 260, 2345-2354, 1985  
A:Title: Human tumor necrosis factor. Production, purification, and characterization  
A:Reference number: A92511; MUID:85130974  
A:Contents: annotation; disulfide bond  
C:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc  
out detriment to normal cells. It can also act synergistically with interferon gamma  
C:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clic  
ut are produced by different cell types and have different induction kinetics.  
C:Genetics:  
A:Gene: GDB:TNF; TNFA  
A:Cross-references: GDB:120441; OMIM:191160  
A:Map position: 6p21.3-6p21.3  
A:Introns: 62/3; 78/1; 94/1  
C:Complex: homotrimer  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine;  
F:1-76/Domain: propeptide #status predicted <PRO>  
F:77-233/Product: tumor necrosis factor #status experimental <MAT>  
F:19,20/Binding site: myristate (Lys) (covalent) #status experimental  
F:81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental  
F:145-177/Disulfide bonds: #status experimental

Query Match 7.9%; Score 133; DB 1; Length 233;  
Best Local Similarity 25.5%; Pred. No. 0.00099;  
Matches 40; Conservative 31; Mismatches 62; Indels 24; Gaps 8;

QY 163 QPFAHLTINATIPSGSHKVSLSWYHDKGAKISN-MTFNSKGLINODGFYLYANIC 221  
DB 87 KPAHVAVN---PQAEGL---QWLNRNALLANGVELRDLQVVPSEGLYISQVL 139  
QY 222 FRHH-ETSGDLATEYLQLMV--YVTK-----TSIKIPSSHTLMKGGSTKWSNSEHFY 273  
DB 140 FRGQCPSTHLLTHTTISRIVSYQTKVLLSAIKSPQRETPEGAAPW-----YE 192  
QY 274 SINVGFFKLSRGEETISVSNPFLD-PQDATYFG 309

A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-230, 'R', 232-235 <RES>  
A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA0457.1; PID:g202083  
R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A:Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor  
A:Reference number: A36696; MUID:91097531  
A:Accession: A36696  
A:Molecule type: protein  
A:Residues: 80-85, 'X', 87-99 <SHE>  
C:Genetics:  
A:Introns: 62/3; 81/1; 97/1  
A:Note: the first intron occurs in the 5'-untranslated region  
C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane  
F:80-235/Product: tumor necrosis factor status experimental <MAT>  
F:80/Binding site: myristate (Lys) (covalent) #status predicted  
F:84/Binding site: carboxylate (Ser) (covalent) #status predicted  
F:86/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:148-179/Disulfide bonds: #status predicted  
Query Match 8.4%; Score 141.5; DB 1; Length 235;  
Best Local Similarity 25.9%; Pred. No. 0.00019;  
Matches 42; Conservative 28; Mismatches 57; Indels 35; Gaps 7;  
QY 163 QPFAHITINATIPSGSHKVSLS-SWYHGRGAKISN-WTFNSGKLIVNODGFYLYANI 220  
DB 90 KPAHVAVN-----HOVEQLEWLSORANALLANGMDLNQVLPADGLYLYISQV 141  
QY 221 CFRHHTSGDLATEYLQLMVYTK-----TSIKIPSSHTLMRGSGTKYWSGNS 268  
DB 142 LFK-----CGCPDYVLLHTVSRFAISYQKVNLLSAVSKPCPKDTPGAEALKPW---- 192  
QY 269 EFHYTSINVGPFKLRSGEISIEVSNPSLLD-PDQATYFG 309  
DB 193 ---YEPIYLGGVFOLEKQDLSAEVNLPKYLDPAESGQVYFG 231  
RESULT 7  
A25451  
tumor necrosis factor alpha precursor - rabbit  
N:Alternate names: cachectin; TNF alpha  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
C:Accession: A25454; A25451; JS0727  
R:Itto, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.  
DNA 5, 149-156, 1986  
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor  
A:Reference number: A25454; MUID:86219711  
A:Accession: A25454  
A:Molecule type: mRNA  
A:Residues: 1-234 <ITO>  
A:Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760  
R:Itto, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.  
DNA 5, 157-165, 1986  
A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.  
A:Reference number: A25451; MUID:86219712  
A:Accession: A25451  
A:Molecule type: DNA  
A:Residues: 1-234 <IT2>  
A:Note: this sequence differs from that shown in having a Gln inserted between residues R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.  
Gene 95, 215-221, 1990  
A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- $\alpha$  and TNF- $\beta$   
A:Reference number: JH0309; MUID:91065534  
A:Accession: JS0727  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-62, 'Q', 63-234 <SHA>  
A:Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756  
C:Genetics:  
A:Introns: 62/3; 80/1; 96/1

C:Superfamily: tumor necrosis factor  
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane  
F:1-81/Domain: propeptide #status predicted <PRO>  
F:82-234/Product: tumor necrosis factor status predicted <MAT>  
F:19/20/Binding site: myristate (Lys) (covalent) #status predicted  
F:83/Binding site: carboxylate (Ser) (covalent) #status predicted  
F:147-178/Disulfide bonds: #status predicted  
Query Match 8.4%; Score 141; DB 1; Length 234;  
Best Local Similarity 21.6%; Pred. No. 0.00021;  
Matches 65; Conservative 35; Mismatches 99; Indels 102; Gaps 13;  
QY 27 EGPLHAPPPAPHPAPASR-----SMFVALIGLIGGVVCSVALFFYFRAQMDPNRISD 82  
DB 14 EGPL-----PKAGGPGSKRCCLSLFSLVAGATLFC-----LLHFRVIGQEEESP 65  
QY 83 GTHCYIVRLRHENADFOTTLTSEODTKLPDSCRIKQAFQAGVOKELQHVGSQHIA 142  
DB 66 NUHLV-----NPVQAWTLRS-----A 82  
QY 143 EKAVDGSWLDLAKRSKLEAQPFAHITINATIPSGSHKVSLSWYHGRGAKISN-WTF 201  
DB 83 SRALSD-----KPLAHVVAN-----PQVEGQL-----OWLSORANALLANGMKL 131  
QY 202 SNGKLIVNODGFYLYANICFRHHTSGDLATEYLQLMVYTKTSIKIPSSHTLMKG--- 258  
DB 122 TDNLQVVPADGLYLYISQVLF-----SGGCRSYVLLTHTVSRFAVSPYKVNLLSAIKS 176  
QY 259 -----GSTKYWSGNESEFHYTSINVGPFKLRSGEISIEVSNPSLLD-PDQATYF 308  
DB 177 PCURETPEEAEPMAW-----YEPIYLGGVFOLEKGRDLSTEVNPEYLDLAESGQVYF 229  
QY 309 G 309  
DB 230 G 230  
RESULT 8  
JH0529  
tumor necrosis factor alpha precursor - sheep  
N:Alternate names: cachectin; TNF alpha  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000  
C:Accession: JH0529; S48118; S13114; S20661  
R:Green, I.R.; Sargan, D.R.  
Gene 109, 203-210, 1991  
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with the sequence  
A:Reference number: JH0529; MUID:92112044  
A:Accession: JH0529  
A:Molecule type: mRNA  
A:Residues: 1-234 <GRE>  
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406  
A:Experimental source: alveolar macrophage  
R:Nash, A.D.; Barclay, G.J.; Brandon, M.R.; Andrews, A.E.  
Immunol. Cell Biol. 69, 273-283, 1991  
A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.  
A:Reference number: S48118; MUID:92155784  
A:Accession: S48118  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-234 <NAS>  
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807  
R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.  
Nucleic Acids Res. 18, 6723, 1990  
A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.  
A:Reference number: S13114; MUID:91067496  
A:Accession: S13114  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-62, 64-234 <YOU>  
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404  
A:Note: comparison with the introns of homologous sequences suggest that this is prot  
C:Superfamily: tumor necrosis factor

QY 238 LMVYTKTSIKIPSSHTLMKGSTKYWSCNSEFFHYFYSINVGGFFKLRSGEISIEVSNPS 297  
 DB- 206 HKVYM-RNFKYPGDLVLMEEKLNCT-TGQIWAHSSYLGAFTVADHLVYNISQLS 262  
 QY 298 LLDPODATTYFCAFKV 313  
 DB 263 LNFEESTFFGLYL 278

## RESULT 5

CD40 ligand - human  
 N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Apr-2001  
 C:Accession: S28017; JH0793; S26694; I53476; S25684; S30593  
 R:Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;  
 BO J. 11, 4313-4321, 1992  
 A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for  
 A:Reference number: S28017; MUID:93049181  
 A:Accession: S28017  
 A:Molecule type: mRNA  
 A:Residues: 1-261 <HO>  
 A:Cross-references: EMBL:Z15017; NID:938483; PIDN:CAA78737.1; PID:938484  
 R:Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.  
 J. Exp. Med. 176, 1543-1550, 1992  
 A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin  
 A:Reference number: JH0793; MUID:93049181  
 A:Accession: JH0793  
 A:Molecule type: mRNA  
 A:Residues: 1-261 <SPR>  
 A:Cross-references: GB:X67878; NID:938411; PIDN:CAA48077.1; PID:938412  
 A:Experimental source: peripheral blood T-cell  
 R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A.  
 Eur. J. Immunol. 22, 3191-3194, 1992  
 A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.  
 A:Reference number: S26694; MUID:93076854  
 A:Accession: S26694  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-261 <GRA>  
 A:Cross-references: EMBL:X68550; NID:937269; PIDN:CAA48554.1; PID:937270  
 R:Gauchat, J.F.; Aubry, J.P.; Mazzel, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.  
 FEBS Lett. 315, 259-266, 1993  
 A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e  
 A:Reference number: S28852; MUID:93138085  
 A:Accession: S28852  
 A:Molecule type: mRNA  
 A:Residues: 1-261 <GAD>  
 A:Cross-references: EMBL:L07414; NID:9180123; PIDN:AAA35662.1; PID:g180124  
 A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln  
 C:Genetics:  
 A:Gene: GDB:CD40LG; HG101; IMD3  
 A:Cross-references: GDB:120632; OMIM:308230  
 A:Map position: Xq26-Xq26  
 C:Keywords: glycoprotein; transmembrane protein  
 F:13-44/Domain: transmembrane #status predicted <TMM>  
 F:45-261/Domain: extracellular #status predicted <EXT>  
 F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 158.5; DB 2; Length 261;  
 Best Local Similarity 24.5%; Pred. No. 8.1e-06;  
 Matches 68; Conservative 53; Mismatches 113; Indels 43; Gaps 15;

QY 45 SRSMFVALLGLGL-GQVCSVALFFPFRQMDPNRISDGTCHYILRLRHENADQDT- 102  
 DB 20 SMKIFMYLTVLTOMIGSALFAVYLHRLD-KIEDE-----RNHEDVFPMKI 69  
 QY 103 -TLESODTKLIPDSCRRIFKQAFQVOKELOHVGSQHIAEKAMVDGSLDLAKRSKLE 161  
 DB 70 QRCNTGERSLSLNCIEIKSQEGFV-KDIM-----LNKEETKKNSEF-EMQKQDQ-N 119

QY 162 AQPFALHTNATDIPSGSHKVSLSWYHGRWAKISN--WTFSGNK-LIVNODGFYLYA 218  
 DB 120 PQIAAHVISEAS-----SKTTSVLQW-AEKGYITMSNNLVLENGKQLTKRQGLYYIA 173  
 QY 219 NICFRHETSGDLATEYLQLMVTVTKTSIKIPS--SHTLMKGSTKYWSCNSEFFHYFYSIN 276  
 DB 174 QVTFCNSRREASSQAP-----FIASLCLKSGRFRILLRANTH--SSARPCGGOOSIN 224  
 QY 277 VGGFFKLRSGEISIEVSNPSLLDPODATTYFCAFKV 313  
 DB 225 LGGVFELOPGASVFNVTDPQSVSHGTGFTSFGLLKL 261

## RESULT 6

QWMSN  
 tumor necrosis factor alpha precursor - mouse  
 N:Alternate names: cachectin; TNF alpha  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 04-Feb-2000  
 C:Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36896  
 R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.  
 DNA 7, 193-201, 1988  
 A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necr  
 A:Reference number: A22908; MUID:88224564  
 A:Accession: A22908  
 A:Molecule type: DNA  
 A:Residues: 1-235 <SH1>  
 A:Cross-references: GB:M20155  
 R:Shakhov, A.N.; Nedospasov, S.A.  
 Bioorg. Khim. 13, 701-705, 1987  
 A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete  
 A:Reference number: S03791; MUID:87298639  
 A:Accession: S03791  
 A:Molecule type: DNA  
 A:Residues: 1-235 <SHA>  
 A:Cross-references: GB:M38296; NID:9202086; PIDN:AAA40459.1; PID:9202087  
 A:Note: article in Russian with English abstract  
 R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.  
 Nucleic Acids Res. 15, 9083-9084, 1987  
 A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor  
 A:Reference number: A93679; MUID:88067722  
 A:Accession: A27303  
 A:Molecule type: DNA  
 A:Residues: 1-235 <SEM>  
 A:Cross-references: GB:Y00467; NID:954830; PIDN:CAA68530.1; PID:954832  
 R:Pennica, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985  
 A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor nec  
 A:Reference number: A25164; MUID:85298296  
 A:Accession: A25164  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <PEN>  
 A:Cross-references: GB:M11731; NID:9202084; PIDN:AAA40458.1; PID:9202085  
 R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashi  
 Nucleic Acids Res. 13, 4417-4429, 1985  
 A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic e  
 A:Reference number: A23127; MUID:85242112  
 A:Accession: A23127  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <FRA>  
 A:Cross-references: GB:X02611; NID:954844; PIDN:CAA26457.1; PID:954845  
 R:Cseh, K.; Beutler, B.  
 J. Biol. Chem. 264, 16256-16260, 1989  
 A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resu  
 A:Reference number: A34251; MUID:89380231  
 A:Accession: A34251  
 A:Molecule type: protein  
 A:Residues: 70-87 <CSE>  
 R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986  
 A:Title: Identification of a common nucleotide sequence in the 3'-untranslated regio  
 A:Reference number: I59058; MUID:86149365  
 A:Accession: I59058



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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 56.3343 Seconds  
(without alignments)  
540.706 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1695  
Sequence: 1 MRRASRDYTKYLRGSEMGG.....LLDPDQATYFGAFKVRDID 317

Scoring table: BLASUM62  
Gapop 10.0 , Gapext 0.5

Archived: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 189   | 11.2        | 281    | 2 I38707 | Fas ligand - human |
| 2          | 184.5 | 10.9        | 279    | 2 A53062 | Fas ligand - mouse |
| 3          | 176.5 | 10.5        | 261    | 2 S53090 | CD40 ligand - bovi |
| 4          | 175.5 | 10.4        | 278    | 2 A49266 | fas ligand - rat   |
| 5          | 158.5 | 9.4         | 261    | 2 I53476 | CD40 ligand - huma |
| 6          | 141.5 | 8.4         | 235    | 1 QWMSN  | tumor necrosis fac |
| 7          | 141   | 8.4         | 234    | 1 A23451 | tumor necrosis fac |
| 8          | 137   | 8.1         | 234    | 1 JH0529 | tumor necrosis fac |
| 9          | 133   | 7.9         | 233    | 1 QWUHN  | tumor necrosis fac |
| 10         | 132.5 | 7.9         | 235    | 2 I54490 | tumor necrosis fac |
| 11         | 131.5 | 7.8         | 235    | 2 J00029 | tumor necrosis fac |
| 12         | 130.5 | 7.7         | 306    | 2 I49139 | lymphotoxin-beta - |
| 13         | 130   | 7.7         | 233    | 1 S22052 | tumor necrosis fac |
| 14         | 128   | 7.6         | 234    | 1 JQ1344 | tumor necrosis fac |
| 15         | 126.5 | 7.5         | 233    | 1 S24642 | tumor necrosis fac |
| 16         | 126   | 7.5         | 232    | 1 S12606 | tumor necrosis fac |
| 17         | 125.5 | 7.4         | 185    | 2 S52715 | tumor necrosis fac |
| 18         | 122   | 7.2         | 193    | 2 S06192 | tumor necrosis fac |
| 19         | 120   | 7.1         | 260    | 2 S21738 | CD40 ligand - mous |
| 20         | 117   | 6.9         | 233    | 2 S11688 | tumor necrosis fac |
| 21         | 117   | 6.9         | 244    | 2 A46066 | lymphotoxin beta - |
| 22         | 97.5  | 5.8         | 1464   | 1 CGHU1S | collagen alpha 1(I |
| 23         | 94.5  | 5.6         | 664    | 2 C84747 | probable protein k |
| 24         | 92.5  | 5.5         | 205    | 1 QWUHX  | lymphotoxin alpha  |
| 25         | 92.5  | 5.5         | 450    | 2 S38114 | hypothetical prote |
| 26         | 91.5  | 5.4         | 3848   | 2 T17414 | TiPC protein - sli |
| 27         | 91    | 5.4         | 493    | 2 AC0937 | probable GntR-fam  |
| 28         | 90.5  | 5.4         | 1694   | 2 S50065 | sialoadhesin - mou |
| 29         | 90    | 5.3         | 730    | 2 JCI456 | gelatinase B (EC 3 |

|    |      |     |      |          |                    |
|----|------|-----|------|----------|--------------------|
| 30 | 89.5 | 5.3 | 331  | 2 AF3526 | homoprotocatechuat |
| 31 | 89.5 | 5.3 | 379  | 2 A47659 | farnesyl-protein t |
| 32 | 89   | 5.3 | 202  | 1 B27303 | tumor necrosis fac |
| 33 | 89   | 5.3 | 440  | 2 I49681 | glyceraldehyde-3-p |
| 34 | 89   | 5.3 | 479  | 2 A25052 | fibrinogen beta ch |
| 35 | 89   | 5.3 | 639  | 2 C83624 | probable two-compo |
| 36 | 88.5 | 5.3 | 565  | 2 C89893 | hypothetical prote |
| 37 | 88.5 | 5.3 | 578  | 2 S51379 | probable phosphoe  |
| 38 | 88.5 | 5.3 | 684  | 2 T01267 | leucine-rich repea |
| 39 | 88.5 | 5.3 | 883  | 2 A49733 | heparan sulfate-N- |
| 40 | 87.5 | 5.2 | 610  | 2 T06690 | galactonolactone d |
| 41 | 87.5 | 5.2 | 1466 | 1 CGHU7L | collagen alpha 1(I |
| 42 | 87   | 5.2 | 639  | 2 A32935 | protein p1 - Entam |
| 43 | 87   | 5.2 | 1114 | 2 JH0284 | 125K surface anti  |
| 44 | 87   | 5.2 | 1315 | 2 G96722 | hypothetical prote |
| 45 | 86.5 | 5.1 | 279  | 2 F72339 | hypothetical prote |

ALIGNMENTS

RESULT 1

I38707  
Fas ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
C:Accession: I38707; JC2340; S57565; I38554  
R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
Int. Immunol. 6, 1567-1574, 1994  
A:Title: Human Fas ligand: gene structure, chromosomal location and species specific  
A:Reference number: I38707; MUID:95127560  
A:Accession: I38707  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RES>  
A:Cross-references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431  
R:Mita, E.; Hayashi, N.; Ito, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A:Reference number: JC2340; MUID:95071350  
A:Accession: JC2340  
A:Molecule type: DNA  
A:Residues: 1-281 <MIT>  
A:Cross-references: GB:D38122; DBJ:D29820; NID:g601892; PIDN:BAA07320.1; PID:g13699  
R:Schatzlein, C.E.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: S57565  
A:Accession: S57565  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-281 <SCH>  
A:Cross-references: EMBL:X89102; NID:g887455; PID:g887456  
R:Allderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A. J. Exp. Med. 181, 71-77, 1995  
A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
A:Reference number: I38554; MUID:95105731  
A:Accession: I38554  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RE2>  
A:Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628  
C:Genetics:  
A:Gene: FasL  
A:Introns: 151/1; 116/3  
C:Keywords: glycoprotein; transmembrane protein  
F:80-102/Domain: transmembrane #status predicted <TMM>  
F:76,184,250,260/Binding site: carbohydrate (Asn) #status predicted

Query Match 11.2%; Score 189; DB 2; Length 281;  
Best Local Similarity 21.7%; Pred. No. 2.4e-08;  
Matches 69; Conservative 43; Mismatches 98; Indels 108; Gaps 11;  
QY 22 PGAPHEGFLHAPPPAP-----HQPRAASRS-----MFVALLGIGIGQVVCVS 63

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (sp  
N:Alternate names: 190K protein; polymorphic schizont antigen  
C:Species: Plasmodium falciparum  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jun-2000  
C:Accession: S06286  
R:Certá, U.; Rotmann, D.; Matile, H.; Reber-Liske, R.  
EMBO J. 6, 4137-4142, 1987  
A:Title: A naturally occurring gene encoding the major surface antigen precursor p190 of  
A:Reference number: S06286; MUID:88166657  
A:Accession: S06286  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-1060 <CER>  
C:Superfamily: major merozoite surface antigen  
C:Keywords: surface antigen

Query Match 57.4%; Score 42.5; DB 2; Length 1060;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 983 QFVKSNSKVITGLTE 997

#### RESULT 7

S16752  
major merozoite surface antigen MSA-1 - malaria parasite (Plasmodium falciparum) (fragme  
N:Alternate names: polymorphic schizont antigen p190  
C:Species: Plasmodium falciparum  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jun-2000  
C:Accession: A44865; S16752  
R:Olafsson, P.; Matile, H.; Certá, U.  
Exp. Parasitol. 74, 381-389, 1992  
A:Title: Plasmodium falciparum: the repetitive MSA-1 surface protein of the RO-71 isolat  
A:Reference number: A44865; MUID:92275047  
A:Accession: A44865  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1086 <OLA>  
A:Cross-references: EMBL:X51930  
A:Experimental source: isolate RO-71  
C:Genetics:  
A:Gene: MSAL  
C:Superfamily: major merozoite surface antigen  
C:Keywords: glycoprotein; merozoite; surface antigen; tandem repeat

Query Match 57.4%; Score 42.5; DB 2; Length 1086;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 1009-QFVKSNSKVITGLTE 1023

#### RESULT 8

A54498  
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (is  
C:Species: Plasmodium falciparum  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C:Accession: A54498  
R:Peterson, M.G.; Coppel, R.L.; McIntyre, P.; Langford, C.J.; Woodrow, G.; Brown, G.V.;  
Mol. Biochem. Parasitol. 27, 291-302, 1988  
A:Title: Variation in the precursor to the major merozoite surface antigens of Plasmodiu  
A:Reference number: A54498; MUID:88142999  
A:Accession: A54498  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1701 <PET>  
A:Cross-references: GB:M19143; NID:g160412; PID:AAA29653.1; PID:g160413  
C:Superfamily: major merozoite surface antigen  
C:Keywords: surface antigen

#### Query Match

57.4%; Score 42.5; DB 2; Length 1701;

Best Local Similarity 60.0%; Pred. No. 30;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 1001 QFVKSNSKVITGLTE 1015

#### RESULT 9

A26868  
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 09-Jun-2000  
C:Accession: A26868  
R:fanabe, K.; Mackay, M.; Coman, M.; Scaife, J.G.  
J. Mol. Biol. 195, 273-287, 1987  
A:Title: Allelic dimorphism in a surface antigen gene of the malaria parasite Plasmo  
A:Reference number: A26868; MUID:88011243  
A:Accession: A26868  
A:Molecule type: DNA  
A:Residues: 1-1701 <TAN>  
C:Superfamily: major merozoite surface antigen  
C:Keywords: signal sequence #status predicted <SIG>  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-1701/Product: major merozoite surface antigen #status predicted <MAT>

#### Query Match

57.4%; Score 42.5; DB 2; Length 1701;

Best Local Similarity 60.0%; Pred. No. 30;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 1 QYIKANSKFI-GITE 14

DB 1001 QFVKSNSKVITGLTE 1015

#### RESULT 10

SAZOGM  
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)  
N:Alternate names: 195K glycoprotein  
C:Species: Plasmodium falciparum  
C:Date: 30-Sep-1987 #sequence\_revision 31-Mar-1991 #text\_change 09-Jun-2000  
C:Accession: A23386; S06361  
R:Weber, J.L.; Leininger, W.M.; Lyon, J.A.  
Nucleic Acids Res. 14, 3311-3323, 1986  
A:Title: Variation in the gene encoding a major merozoite surface antigen of the hum  
A:Reference number: A23386; MUID:86205236  
A:Accession: A23386  
A:Molecule type: DNA  
A:Residues: 1-1104 <WEB1>  
A:Cross-references: EMBL:X03831  
R:Weber, J.L.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.  
Nucleic Acids Res. 16, 1206, 1988  
A:Title: Merozoite surface protein sequence from the Camp strain of the human malari  
A:Reference number: S06361; MUID:88143999  
A:Accession: S06361  
A:Molecule type: DNA  
A:Residues: 1104-1726 <WEB2>  
A:Cross-references: EMBL:X03831  
C:Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. Th  
C:Superfamily: major merozoite surface antigen  
C:Keywords: glycoprotein; merozoite; surface antigen; tandem repeat  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-1726/Product: major merozoite surface antigen #status predicted <MAT>  
F:67-87,91-96,100-105,109-120/Region: 3-residue repeats (S-G-F)  
F:757-765/Region: 3-residue repeats (T-E-E)  
F:133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: car

#### Query Match

57.4%; Score 42.5; DB 1; Length 1726;

Best Local Similarity 60.0%; Pred. No. 31;

Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;





Thu Oct 10 16:31:18 2002

us-09-787-126-34.rpr

Page 5

QY 1 QYIKANSKEFIGITE 14  
Db 124 QYITSNATFTGISE 137

Search completed: October 10, 2002, 15:59:14  
Job time : 5.66566 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 2.66566 Seconds  
(without alignments)  
540.706 Million cell updates/sec

Title: US-09-787-126-34

Perfect score: 74

Sequence: 1 QVIKANSKFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Aligned: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 74    | 100.0       | 1315   | 1 BTCLTN | tentoxylisin (EC 3 |
| 2          | 44.5  | 60.1        | 244    | 2 S29982 | class II histocomp |
| 3          | 44    | 59.5        | 66     | 2 S31029 | gene 84 protein -  |
| 4          | 43    | 58.1        | 180    | 2 G86826 | diamine N-acetyltr |
| 5          | 43    | 58.1        | 899    | 2 T42976 | hypothetical prote |
| 6          | 42.5  | 57.4        | 1060   | 2 S06286 | major merozoite su |
| 7          | 42.5  | 57.4        | 1086   | 2 S16752 | major merozoite su |
| 8          | 42.5  | 57.4        | 1701   | 2 A54498 | major merozoite su |
| 9          | 42.5  | 57.4        | 1701   | 2 A26868 | major merozoite su |
| 10         | 42.5  | 57.4        | 1726   | 1 SAZQCM | major merozoite su |
| 11         | 42.5  | 57.4        | 1726   | 2 A45948 | blastopia polyprot |
| 12         | 42    | 56.8        | 1333   | 2 S38635 | Ig heavy chain V-D |
| 13         | 41    | 55.4        | 123    | 2 G48677 | siderophore/surfac |
| 14         | 41    | 55.4        | 447    | 2 H97146 | hypothetical prote |
| 15         | 41    | 55.4        | 899    | 2 G36812 | class II histocomp |
| 16         | 40.5  | 54.7        | 245    | 2 S29980 | hypothetical prote |
| 17         | 40    | 54.1        | 79     | 2 D85794 | lacyl-carrier-prot |
| 18         | 40    | 54.1        | 194    | 2 G64026 | oligopeptidase (EC |
| 19         | 40    | 54.1        | 601    | 1 A55485 | oligoendopeptidase |
| 20         | 40    | 54.1        | 601    | 2 G86840 | hypothetical prote |
| 21         | 40    | 54.1        | 644    | 2 S46746 | Ig heavy chain V r |
| 22         | 39    | 52.7        | 102    | 2 PH1491 | Ig heavy chain V r |
| 23         | 39    | 52.7        | 119    | 2 PH1516 | Ig heavy chain V r |
| 24         | 39    | 52.7        | 119    | 2 PH1518 | Ig heavy chain V r |
| 25         | 39    | 52.7        | 119    | 2 PH1519 | Ig heavy chain V-D |
| 26         | 39    | 52.7        | 123    | 2 F48677 | Ig heavy chain V r |
| 27         | 39    | 52.7        | 135    | 2 PH1494 | Ig heavy chain V r |
| 28         | 39    | 52.7        | 140    | 2 PH1488 | conserved hypothet |
| 29         | 39    | 52.7        | 189    | 2 G97978 |                    |

adenylate kinase ( type II restrictio  
probable acetyl-Co  
type IIS restricti  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
trNA-pseudouridine  
probable hexosyltr  
hypothetical prote  
endo-1,4-beta gluc  
cellulase (EC 3.2.  
methyl-accepting c  
hemagglutinin-neur

## ALIGNMENTS

### RESULT 1

BTCLTN tentoxylisin (EC 3.4.24.68) precursor - Clostridium tetani

N:Alternate names: tetanus neurotoxin

C:Species: Clostridium tetani

C:Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 18-Jun-1999

C:Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364

R:Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel

EMBO J. 5, 2495-2502, 1986

A:Title: Tetanus toxin: primary structure, expression in E. coli, and homology with

A:Reference number: A25689; MUID:87053814

A:Accession: A25689

A:Molecule type: DNA

A:Residues: 1-1315 <EIS>

A:Cross-references: GB:X04436; NID:g40769; PIDN:CAA28033.1; PID:g40770

R:Fairweather, N.F.; Lyness, V.A.

Nucleic Acids Res. 14, 7809-7812, 1986

A:Title: The complete nucleotide sequence of tetanus toxin.

A:Reference number: A25757; MUID:87040747

A:Accession: A25757

A:Molecule type: DNA

A:Residues: 1-1315 <FAI>

A:Cross-references: GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g40774

A:Experimental source: strain CN3911

R:Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.

J. Bacteriol. 163, 21-27, 1986

A:Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C

A:Reference number: A25194; MUID:86085672

A:Accession: A25194

A:Molecule type: DNA

A:Residues: 743-1315 <FA2>

A:Cross-references: GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:g144921

A:Accession: B25194

A:Molecule type: protein

A:Residues: 865-894 <FA3>

R:Matsumoto, M.; Iel, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.

Infect. Immun. 57, 3588-3593, 1989

A:Title: Isolation, purification, and characterization of fragment B, the NH-2-termi

A:Reference number: A60759; MUID:90035436

A:Accession: A60759

A:Molecule type: protein

A:Residues: 461-475 <MA>

R:Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Wildmann, C.; Corradin, G.

J. Immunol. 142, 394-402, 1989

A:Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.

A:Reference number: JS0098; MUID:89093918

A:Contents: annotation; epitope region

R:Schiaivo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta,

Nature 359, 832-835, 1992

A:Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by prote

A:Reference number: B27125; MUID:93063293

A:Contents: annotation

R:de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.  
Eur. J. Biochem. 229, 61-69, 1995  
A:Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.  
A:Reference number: S69348; MUID:95262688  
A:Accession: S69348  
A:Molecule type: protein  
A:Residues: 2-31 <DEF>  
C:Comment: The source of this protein was an extrachromosomal plasmid.  
C:Comment: The precursor is cleaved by endogenous proteinase activity to form light (fra  
dual chains are not toxic when separated). The amino end of the heavy chain (fragment B)  
C:Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to ganglio  
C:Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized  
presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy  
C:Function:  
A:Description: blocks neuroexcitotoxicity via hydrolysis of a Gln-Phe peptide bond in synapt  
C:Superfamily: tetanus toxin  
C:Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc  
F:2-457/Product: tetroxylisin light chain (fragment A) #status predicted <TTL>  
F:461-1315/Product: tetroxylisin heavy chain (fragment B.C) #status experimental <TTH>  
F:461-864/Domain: channel forming (fragment B) #status predicted <TXB>  
F:865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>  
F:233,237/Binding site: zinc (His) #status predicted  
234/Active site: Glu #status predicted

Query Match 100.0%; Score 74; DB 1; Length 1315;  
Best Local Similarity 100.0%; Pred. No. 3.6e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 830 QYIKANSKFIGITEL 844  
|||||

# RESULT 2

S29982  
class II histocompatibility antigen - Atlantic salmon  
C:Species: Salmo salar (Atlantic salmon)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Sep-1999  
C:Accession: S29982

R:Hardvik, I.  
submitted to the EMBL Data Library, October 1992

A:Reference number: S29980  
A:Accession: S29982  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-244 <HOR>  
A:Cross-references: EMBL:X70166; NID:g64369; PID:g64370  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 60.1%; Score 44.5; DB 2; Length 244;  
Best Local Similarity 55.6%; Pred. No. 1.8;  
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 QYIKANS---KFIGITEL 15  
DB 51 EYIRFNSVCKFGVGYTEL 58  
||| || ||| |||

# RESULT 3

S31029  
gene 84 protein - Mycobacterium phage L5  
C:Species: Mycobacterium phage L5  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 08-Oct-1999  
C:Accession: S31029  
R:Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.  
Mol. Microbiol. 7, 407-417, 1993  
A:Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans  
A:Reference number: S30949; MUID:93211283  
A:Accession: S31029  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-66 <DON>  
A:Cross-references: EMBL:Z18946; NID:g15859; PIDN:CAA79460.1; PID:e59702; PID:g579152

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
C:Genetics:  
A:Gene: 84  
A:Start codon: GTG

Query Match 59.5%; Score 44; DB 2; Length 66;  
Best Local Similarity 57.1%; Pred. No. 0.58;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 YIKANSKFIGITEL 15  
DB 50 YIKRNGKFGVTWEV 63  
||| ||| |||

# RESULT 4

G86826  
diamine N-acetyltransferase (EC 2.3.1.57) [imported] - Lactococcus lactis subsp. lact  
N:Alternate names: spermidine acetyltransferase  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: G86826  
R:Botolin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissbach, J.; E  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: G86826  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-180 <STO>  
A:Cross-references: GB:AE005176; PID:g12724622; PIDN:AAK05713.1; GSPDB:GN00146  
A:Experimental source: strain ILL1403  
C:Genetics:  
A:Gene: yqfF  
C:Keywords: acyltransferase; coenzyme A

Query Match 58.1%; Score 43; DB 2; Length 180;  
Best Local Similarity 69.2%; Pred. No. 2.5;  
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 IKANSKFIGITEL 15  
DB 65 IEANDTFFIGIVEL 77  
|:| | | | | | | |

# RESULT 5

T42976  
hypothetical protein 63 - ateline herpesvirus 3 (strain 73)  
C:Species: ateline herpesvirus 3  
A:Variety: strain 73  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
C:Accession: T42976  
R:Albrecht, J.C.; Fleckenstein, B.  
submitted to the EMBL Data Library, August 1998  
A:Description: Primary structure of the herpesvirus ateles genome.  
A:Reference number: Z22274  
A:Accession: T42976  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-899 <ALB>  
A:Cross-references: EMBL:AF083424; PIDN:AAC95587.1  
A:Experimental source: strain 73

Query Match 58.1%; Score 43; DB 2; Length 899;  
Best Local Similarity 64.3%; Pred. No. 13;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITE 14  
DB 124 QYITSNFTGTGTE 137  
||| ||| ||| |||

# RESULT 6

S06286

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 : Search time 84.9789 Seconds  
(without alignments)  
414.343 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEMG.....LLDPDQDQYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

arched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802.\*  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID       | Description           |
|------------|--------|-------------|--------|----------|-----------------------|
| 1          | 1685   | 100.0       | 317    | AAW83195 | Human osteoprotegerin |
| 2          | 1685   | 100.0       | 317    | AAW69957 | NF-kB receptor act    |
| 3          | 1685   | 100.0       | 317    | AAW68293 | NF-kB receptor act    |
| 4          | 1685   | 100.0       | 317    | AAW84417 | Amino acid sequenc    |
| 5          | 1685   | 100.0       | 317    | AAW08738 | Human receptor act    |
| 6          | 1685   | 100.0       | 317    | AAE04426 | Human receptor act    |
| 7          | 1685   | 100.0       | 317    | AAE01993 | Human full-length     |
| 8          | 1677   | 99.5        | 317    | AAW83018 | Osteoclastogenesis    |
| 9          | 1417.5 | 84.1        | 316    | AAW83194 | Human osteoprotege    |
| 10         | 1417.5 | 84.1        | 316    | AAW83017 | Osteoclastogenesis    |
| 11         | 1417.5 | 84.1        | 316    | AAW59654 | Amino acid sequenc    |

|    |        |      |     |          |                    |
|----|--------|------|-----|----------|--------------------|
| 12 | 1417.5 | 84.1 | 316 | AAW17874 | Murine TRANCE. Mu  |
| 13 | 1417.5 | 84.1 | 316 | AAW91024 | Mouse OBM protein  |
| 14 | 1417.5 | 84.1 | 316 | AAW84418 | Amino acid sequenc |
| 15 | 1417.5 | 84.1 | 316 | AAW84419 | Amino acid sequenc |
| 16 | 1396.5 | 82.9 | 318 | AAW82092 | Rat osteoclast dif |
| 17 | 1326.5 | 78.7 | 294 | AAW69956 | NF-kB receptor act |
| 18 | 1326.5 | 78.7 | 294 | AAW68292 | NF-kB receptor act |
| 19 | 1326.5 | 78.7 | 294 | AAW08737 | Murine receptor ac |
| 20 | 1326.5 | 78.7 | 294 | AAE04425 | Murine receptor ac |
| 21 | 1326.5 | 78.7 | 294 | AAE01992 | Murine RANKL (rece |
| 22 | 1294   | 76.8 | 246 | AAW83020 | Osteoclastogenesis |
| 23 | 1293   | 76.7 | 245 | AAW17873 | Human TRANCE. Hom  |
| 24 | 1136   | 67.4 | 501 | AAW84420 | Amino acid sequenc |
| 25 | 1109   | 65.8 | 244 | AAW83019 | A murine OCIF-bind |
| 26 | 852    | 50.6 | 160 | AAW08273 | Amino acid sequenc |
| 27 | 814    | 48.3 | 152 | AAW67248 | Human RANKL. Homo  |
| 28 | 790    | 46.9 | 170 | AAW08386 | Mouse FLAG-murine  |
| 29 | 771    | 45.8 | 187 | AAW84420 | Amino acid sequenc |
| 30 | 769    | 45.6 | 173 | AAW84421 | Amino acid sequenc |
| 31 | 768    | 45.6 | 160 | AAW08272 | Amino acid sequenc |
| 32 | 759    | 45.0 | 173 | AAW84422 | A murine osteoprot |
| 33 | 721.5  | 42.8 | 188 | AAW84423 | An osteoprotegerin |
| 34 | 711.5  | 42.2 | 182 | AAW84424 | An osteoprotegerin |
| 35 | 691    | 41.0 | 173 | AAW84425 | DNA encoding osteo |
| 36 | 683    | 40.5 | 139 | AAW91023 | Mouse OBM protein  |
| 37 | 670    | 39.8 | 173 | AAW84426 | An osteoprotegerin |
| 38 | 317.5  | 18.8 | 74  | AAW91020 | Mouse OBM protein  |
| 39 | 252.5  | 15.0 | 281 | AAW27016 | Human Apo-2 ligand |
| 40 | 252.5  | 15.0 | 281 | AAW27017 | Human Apo-2 ligand |
| 41 | 251.5  | 14.9 | 279 | AAW76332 | Human TL2 (TRAIL), |
| 42 | 251.5  | 14.9 | 279 | AAW95032 | Tumour necrosis fa |
| 43 | 251.5  | 14.9 | 281 | AAW27134 | Human Apoptosis in |
| 44 | 251.5  | 14.9 | 281 | AAW19787 | Human Apoptosis in |
| 45 | 251.5  | 14.9 | 281 | AAW19777 | Novel cytokine Apo |

## ALIGNMENTS

RESULT 1  
AAW83195

ID AAW83195 standard; Protein: 317 AA.

XX AAW83195;

DT 11-FEB-1999 (first entry)

Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.  
Human: osteoprotegerin binding protein; OPG binding protein; arthritis;  
osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;  
hypercalcaemia; osteoclast differentiation and activation receptor;  
Paget's disease.

OS Homo sapiens.

PN WO9846751-A1.

PD 22-OCT-1998.

XX 15-APR-1998; 98WO-US07584.

XX 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

PA (AMGE-) AMGEN INC.

XX Boyle WJ;

PI WPI; 1998-594578/50.

DR N-PSDB; AAV70285.

XX

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,  
 PT e.g. treating bone diseases by modulating osteoclast differentiation  
 PT and for diagnosis  
 XX  
 PS Claim 19; Fig 4; 47pp; English.  
 XX  
 CC The present sequence is human osteoprotegerin (OPG) binding protein.  
 CC Host cells transfected with vectors containing nucleic acid molecules  
 CC encoding OPG binding protein are used to produce recombinant OPG binding  
 CC protein. OPG binding protein is used in binding assays to determine  
 CC osteoprotegerin (OPG) in biological samples; to screen for specific  
 CC binding agents (particularly agonists and antagonists, including  
 CC intracellular proteins); to raise Ab (useful in immunoassays for  
 CC detection of OPG binding protein) and to identify compounds that  
 CC modulate binding of OPG binding protein to osteoclast differentiation  
 CC and activation receptor (OAR). The nucleic acid molecule encoding OPG  
 CC binding protein can be used to detect OPG binding protein-encoding  
 CC sequences, e.g. screening for related sequences, also to produce  
 CC transgenic animal models, while complementary sequences are used for  
 CC antisense regulation of OPG binding protein expression. Modulators of  
 CC OPG binding protein, particularly soluble forms of OPG binding protein  
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,  
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's  
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,  
 CC optionally in combination with agents that promote bone growth.

XX Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 19; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEMGCGCAPHEGPHAPPAPPPAPPAASRMFVALLGLGQV 60  
 DB 1 MRRASRDYTKYLRGSEMGCGCAPHEGPHAPPAPPPAPPAASRMFVALLGLGQV 60  
 QY 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 DB 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 QY 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPFAHLTINATDIPSGSH 180  
 DB 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPFAHLTINATDIPSGSH 180  
 QY 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 DB 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSFEHFYSINVGFFKLRSGEETSIIEVSNPSLLD 300  
 DB 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSFEHFYSINVGFFKLRSGEETSIIEVSNPSLLD 300  
 QY 301 PQDATYFGAFKVRDID 317  
 DB 301 PQDATYFGAFKVRDID 317

RESULT 2

AAW69957  
 ID AAW69957 standard; Protein; 317 AA.  
 XX  
 AC AAW69957;  
 XX  
 DT 08-OCT-1998 (first entry)  
 XX  
 DE NF-kB receptor activator RANK ligand (RANKL).  
 XX  
 KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
 KW immune response; inflammatory response; toxic shock; sepsis;  
 KW RANKL; RANK ligand; tumour necrosis factor; TNF.  
 XX  
 OS Homo sapiens.

PN WO9828426-A2.  
 XX  
 PD 02-JUL-1998.  
 XX  
 PF 22-DEC-1997; 97WO-US23775.  
 XX  
 PR 14-OCT-1997; 97US-0064671.  
 PR 23-DEC-1996; 96US-0059978.  
 PR 07-MAR-1997; 97US-0813509.  
 XX  
 PA (IMV) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Galibert LJ, Maraskovsky E;  
 XX  
 DR WPI: 1998-377657/32.  
 DR N-PSDB; AAV41378.  
 XX  
 PT New isolated ligand for receptor activator of NF-kappa B - used to  
 PT develop products for augmenting an immune response for inhibiting an  
 PT inflammatory response and for protection of cells  
 XX  
 PS Claim 27; Pages 59-60; 80pp; English.  
 XX  
 CC This represents a human RANKL, a ligand for the RANK (receptor  
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a  
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK  
 CC may be used for inhibiting activation of NF-kB, by contacting a cell  
 CC expressing membrane-associated RANK with a soluble RANK which binds to  
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be  
 CC used to induce maturation of dendritic cells and enhance their  
 CC allo-stimulatory capacity, thereby augmenting an immune response. The  
 CC soluble RANK polypeptide composition may also be used for regulating an  
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists  
 CC may be useful in ameliorating negative effects of an inflammatory  
 CC response that result from triggering of RANK, e.g. in treating toxic  
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory  
 CC reactions. They can also be used in adjunct therapy for disease  
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides  
 CC can also be used to identify inhibitors of RANK and thus inhibitors of  
 CC an inflammatory response, and also for protecting RANK-expressing cells  
 CC from the negative effects of chemotherapy or the presence of high levels  
 CC of TNF-alpha. The products can also be used for detection and drug  
 CC screening.

XX Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 19; Length 317;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-156;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRGSEMGCGCAPHEGPHAPPAPPPAPPAASRMFVALLGLGQV 60  
 DB 1 MRRASRDYTKYLRGSEMGCGCAPHEGPHAPPAPPPAPPAASRMFVALLGLGQV 60  
 QY 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 DB 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120  
 QY 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPFAHLTINATDIPSGSH 180  
 DB 121 QAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAPFAHLTINATDIPSGSH 180  
 QY 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 DB 181 KVSLSWYHNRGWAKISNMTFSGKLIYVNDGFYILYANICFRHHTSGDLATEYLQLMV 240  
 QY 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSFEHFYSINVGFFKLRSGEETSIIEVSNPSLLD 300  
 DB 241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSFEHFYSINVGFFKLRSGEETSIIEVSNPSLLD 300  
 QY 301 PQDATYFGAFKVRDID 317  
 DB 301 PQDATYFGAFKVRDID 317

|          |  |   |     |
|----------|--|---|-----|
| DB       | 121  | QAFQGVAVQELQHIVGSHIRAEKAWDGSWLDLAKRSKLEAQFAHLLTNATDIPSGSH     | 180 |
| QY       | 181  | KVSLSSWYHNRGWAKISNNMTFSGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLMV   | 240 |
| DB       | 181  | KVSLSSWYHNRGWAKISNNMTFSGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLMV   | 240 |
| QY       | 241  | YVTKTSIKIPSSHTLMKGGSTKYWGSNSEFHYPHSYINWGGFFKLRSGEISIEVSNPSLLD | 300 |
| DB       | 241  | YVTKTSIKIPSSHTLMKGGSTKYWGSNSEFHYPHSYINWGGFFKLRSGEISIEVSNPSLLD | 300 |
| QY       | 301  | PQDQATYFGAKFVRDID 317   |     |
| DB       | 301  | PQDQATYFGAKFVRDID 317   |     |
| RESULT 4 |  |   |     |
| AAY84417 |  |   |     |
| ID       | AAY84417 standard; Protein; 317 AA.                                      |   |     |
| XX       | AC   | AAY84417;   |     |
| XX       | XX   |   |     |
| DT       | 25-JUL-2000 (first entry)  |   |     |
| XX       | Amino acid sequence of a human osteoprotegerin ligand (OPGL).            |   |     |
| XX       | Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;       |   |     |
| KW       | tumour necrosis factor receptor; type II transmembrane protein;          |   |     |
| KW       | osteoclast differentiation; CSF-1; osteoclast activator;                 |   |     |
| KW       | immune response; osteoporosis; bone resorption.                          |   |     |
| XX       |  |   |     |
| OS       | Homo sapiens.  |   |     |
| XX       | Key  | Location/Qualifiers   |     |
| PH       | Region   | 49..69  |     |
| FT       |  | /note= "transmembrane region"                                 |     |
| FT       | Domain   | 70..157   |     |
| FT       |  | /note= "extracellular stalk domain"                           |     |
| FT       | Region   | 158..317  |     |
| FT       |  | /note= "active ligand-moiety"                                 |     |
| XX       |  |   |     |
| PN       | W0200015807-A1.  |   |     |
| XX       |  |   |     |
| PD       | 23-MAR-2000.   |   |     |
| XX       |  |   |     |
| PF       | 13-SEP-1999; 99WO-DK00481.   |   |     |
| XX       |  |   |     |
| PR       | 15-SEP-1998; 98DK-0001164.   |   |     |
| PR       | 02-OCT-1998; 98US-0102896.   |   |     |
| XX       |  |   |     |
| PA       | (MEBI-) M & E BIOTECH AS.  |   |     |
| XX       |  |   |     |
| PI       | Halkier T, Haaning J;  |   |     |
| XX       |  |   |     |
| DR       | WPI; 2000-271444/23.   |   |     |
| DR       | N-PSDB; AAZ99964.  |   |     |
| XX       |  |   |     |
| PT       | In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used   |   |     |
| PT       | to treat, prevent and ameliorate osteoporosis -                          |   |     |
| XX       |  |   |     |
| PS       | Claim 19; Page 78-79; 11Opp; English.                                    |   |     |
| XX       |  |   |     |
| CC       | The present sequence represents a human osteoprotegerin ligand (OPGL).   |   |     |
| CC       | Osteoprotegerin is a secreted member of the tumour necrosis factor       |   |     |
| CC       | receptor family, which blocks osteoclastogenesis in a dose dependent     |   |     |
| CC       | manner. The OPGL protein is synthesised as a type II transmembrane       |   |     |
| CC       | protein. The murine and human OPGL polypeptides are 87% homologous. OPGL |   |     |
| CC       | is a potent osteoclast differentiation factor when combined with CSF-1.  |   |     |
| CC       | It is not capable of inducing osteoclast differentiation in the absence  |   |     |
| CC       | of CSF-1. OPGL is also an activator of mature osteoclasts. The           |   |     |
| CC       | specification describes a method for the in vivo down-regulation of      |   |     |
| CC       | OPGL activity in an animal. The method comprises using at least one OPGL |   |     |
| CC       | polypeptide or subsequence, and/or at least one OPGL analogue to induce  |   |     |
| CC       | an immune response in the animal. The method and OPGL polypeptide are    |   |     |

CC useful for treating, preventing and ameliorating osteoporosis or other  
CC diseases or conditions characterised by excessive bone resorption.  
XX

XX SO Sequence 317 AA;  
Query Match 100.0%; Score 1685; DB 21; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.6e-156;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGPGAPHEGLHAPPAPHPAPPAASRSMFVALLGLGLGV 60  
Db 1 MRRASRDYTKYLRGSEEMGGPGAPHEGLHAPPAPHPAPPAASRSMFVALLGLGLGV 60  
Qy 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSRRIK 120  
Db 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSRRIK 120  
Qy 121 QAFQAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
Db 121 QAFQAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 180  
181 KVSLSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSQDLATEYLQLMV 240  
Db 181 KVSLSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSQDLATEYLQLMV 240  
Qy 241 VYTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYFINVGGFFKLRSGEISIEVSNPSLLD 300  
Db 241 VYTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYFINVGGFFKLRSGEISIEVSNPSLLD 300  
Qy 301 PQDATYFGAFKVRDID 317  
Db 301 PQDATYFGAFKVRDID 317

RESULT 5  
AAE08738  
ID AAE08738 standard; Protein; 317 AA.

XX AC AAE08738;

XX DT 15-NOV-2001 (first entry)

XX DE Human receptor activator of NF kappaB ligand (RANKL) protein.

XX KW Human: receptor activator of nuclear factor kappaB ligand; RANKL; NF;  
KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;  
KW immune response; inflammatory response; graft-versus-host reaction;  
KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;  
KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.

XX KW Homo sapiens.

PN US271349-B1.

XX PD 07-AUG-2001.

XX PF 17-DEC-1998; 98US-0215649.

XX PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0077181.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0772330.

PR 07-MAR-1997; 97US-0813509.

PR 22-DEC-1997; 97US-0996139.

XX (IMM ) IMMUNEX CORP.

XX PI Dougal WC, Galibert L;

XX WPI: 2001-520313/57.

XX DR N-PSDB; AAD15311.

XX PT New receptor activator of NF-kappaB (RANK) polypeptides, useful for

PT

PT express RANK

XX Example 15; Column 71-72; 47pp; English.

XX The patent discloses novel receptor activator of nuclear factor (NF)-  
kappaB (RANK) proteins and their corresponding DNAs. RANK is a member  
of the tumour necrosis factor (TNF) receptor superfamily and associates  
with TNF receptor associated factor (TRAF) 2 and 3 which are important  
in the regulation of immune and inflammatory response. The receptors  
are useful for regulating immune response and in screening for inhibitors  
of these receptors. The cytoplasmic domain of RANK is used in developing  
assays for inhibitors of signal transduction, e.g. for screening the  
molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,  
TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists  
are useful in ameliorating the negative effects of an inflammatory  
response that result from triggering of RANK, e.g. in treating toxic  
shock or sepsis, graft-versus-host reactions, acute inflammatory  
reactions and the effects of bone resorption. RANK acts as an anti-  
apoptotic signal and rescue the cells that express RANK from apoptosis.  
Soluble forms of the receptor are used in vivo or in vitro based  
screening tests for agonists or antagonists of RANK activity, as  
antagonists of RANK-mediated NF-kappa B activation, or to inhibit  
transduction of a signal via RANK. RANK compositions are used in the  
development of both agonistic and antagonistic antibodies, or as an  
adjunct therapy for disease characterised by neoplastic cells that  
express RANK. Compounds that interfere with RANK/TRAF6 interactions  
are useful for modulating the formation of osteoclasts from osteoclast  
precursors and for modulating osteoclast function and activities. They  
are used as inhibitors of diseases associated with excess bone resorption  
and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are  
useful for the expression of recombinant proteins, as probes for analysis  
of the presence or distribution of RANK transcripts, while the proteins  
are useful in preparing kits for the detection of soluble RANK, or  
monitor RANK-related activity. The present sequence is RANK ligand  
(RANKL) protein from human.

XX Sequence 317 AA;

Query Match 100.0%; Score 1685; DB 22; Length 317;  
Best Local Similarity 100.0%; Pred. No. 2.6e-156;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYTKYLRGSEEMGGPGAPHEGLHAPPAPHPAPPAASRSMFVALLGLGLGV 60

Db 1 MRRASRDYTKYLRGSEEMGGPGAPHEGLHAPPAPHPAPPAASRSMFVALLGLGLGV 60

Qy 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSRRIK 120

Db 61 VCSVALFFYFRAQMDPNRISEDTGTHCIYRILRLHENADFQDTTLESQDTKLIPDSRRIK 120

Qy 121 QAFQAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Db 121 QAFQAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy 181 KVSLSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSQDLATEYLQLMV 240

Db 181 KVSLSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSQDLATEYLQLMV 240

Qy 241 VYTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYFINVGGFFKLRSGEISIEVSNPSLLD 300

Db 241 VYTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYFINVGGFFKLRSGEISIEVSNPSLLD 300

Qy 301 PQDATYFGAFKVRDID 317

Db 301 PQDATYFGAFKVRDID 317

RESULT 6

AAE04426

ID AAE04426 standard; Protein; 317 AA.

XX







DR WPI; 1998-594578/50.  
 DR N-PSDB; AAV70284.  
 XX Nucleic acid encoding osteoprotegerin binding protein - useful for,  
 PT e.g. treating bone diseases by modulating osteoclast differentiation  
 PT and for diagnosis  
 XX  
 XX Claim 19; Fig 1; 47pp; English.  
 XX  
 XX The present sequence is human osteoprotegerin (OPG) binding protein.  
 CC Host cells transfected with vectors containing nucleic acid molecules  
 CC encoding OPG binding protein are used to produce recombinant OPG binding  
 CC protein. OPG binding protein is used in binding assays to determine  
 CC osteoprotegerin (OG) in biological samples; to screen for specific  
 CC binding agents (particularly agonists and antagonists, including  
 CC intracellular proteins); to raise Ab (useful in immunoassays for  
 CC detection of OPG binding protein) and to identify compounds that  
 CC modulate binding of OPG binding protein to osteoclast differentiation  
 CC and activation receptor (CDAR). The nucleic acid molecule encoding OPG  
 CC binding protein can be used to detect OPG binding protein-encoding  
 CC sequences, e.g. screening for related sequences, also to produce  
 CC transgenic animal models, while complementary sequences are used for  
 CC antisense regulation of OPG binding protein expression. Modulators of  
 CC OPG binding protein, particularly soluble forms of OPG binding protein  
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,  
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's  
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,  
 CC optionally in combination with agents that promote bone growth.  
 XX  
 XX Sequence 316 AA;  
 XX  
 XX Query Match 84.1%; Score 1417.5; DB 19; Length 316;  
 XX Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 XX Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
 QY 1 MRRASRDYTKYLRSGEMGGPCAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 59  
 DB 1 MRRASRDYTKYLRSGEMGGPCAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 60  
 QY 60 VVCSVALFFYFRAQMDPNRISDGTCHYIRLRLHENADFDQTTLESQDTKLIPDSCRRI 119  
 DB 61 VVCSIALFLYFRAQMDPNRISDGTCHYIRLRLHENAGLDSTLESDT--LPDSCRM 118  
 QY 120 KQAFQAVQKELQHVGSQHIRAEKAWDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179  
 DB 119 KQAFQAVQKELQHVGSQHIRAEKAWDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 178  
 QY 180 HKVSLSSWYHDSGAWKISNNTFSGNKLIVNODGFYLYANICFRHHTSGDLATYQLQM 239  
 DB 179 HKVTLSSWYHDSGAWKISNNTFSGNKLIVNODGFYLYANICFRHHTSGDLATYQLQM 238  
 QY 240 VVYVTKTSIKIPSSHTLMKGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VVYVTKTSIKIPSSHTLMKGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 298  
 QY 300 DPQDATYFGAFKVRDID 317  
 DB 299 DPQDATYFGAFKVRDID 316  
 RESULT 10  
 ID AAW83017 standard; Protein; 316 AA.  
 AC AAW83017;  
 XX  
 XX 10-FEB-1999 (first entry)  
 XX Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).  
 DE Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;  
 KW Osteoclast; bone absorption factor; bone disorder; calcium metabolism.  
 XX

OS Unidentified.  
 PN W09846644-AI.  
 XX  
 XX 22-OCT-1998.  
 PD  
 XX  
 XX 15-APR-1998; 98WO-JP01728.  
 PF  
 XX  
 XX 02-DEC-1997; 97JP-0332241.  
 PR  
 XX 15-APR-1997; 97JP-0097808.  
 PR  
 XX 09-JUN-1997; 97JP-0151434.  
 PR  
 XX 12-AUG-1997; 97JP-0217897.  
 PR  
 XX 21-AUG-1997; 97JP-0224803.  
 XX  
 XX (SNOW) SNOW BRAND MILK PROD CO LTD.  
 PA  
 XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;  
 XX Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;  
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;  
 PI  
 XX WPI; 1998-594563/50.  
 DR N-PSDB; AAV69886.  
 DR  
 XX Protein binding to osteoclastogenesis inhibitory factor - useful  
 PT for, e.g. treatment and investigation of disorders of bone and  
 PT calcium metabolism  
 XX  
 XX Claim 8; Pages 106-108; 151pp; Japanese.  
 XX  
 XX The present sequence represents an osteoclastogenesis inhibitory factor  
 CC (OCIF)-binding molecule (OBM). The protein promotes and supports the  
 CC separation and maturation of osteoclasts in the presence of bone  
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).  
 CC OBM is isolated from stroma cells cultured in the presence of a bone  
 CC absorption factor by separation and solubilisation of membrane proteins  
 CC then affinity chromatography using OCIF. It exists in a full-sequence  
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be  
 CC used for screening potential inhibitors and modifiers of its biological  
 CC activity, and screening for receptors to OBM which mediate its function.  
 CC These substances can then be used in the treatment of disorders of bone  
 CC function and calcium metabolism. The antibodies can be used for assay  
 CC of the protein, for investigative and diagnostic purposes, and as  
 CC components of drugs.  
 XX  
 XX Sequence 316 AA;  
 XX  
 XX Query Match 84.1%; Score 1417.5; DB 19; Length 316;  
 XX Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 XX Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
 QY 1 MRRASRDYTKYLRSGEMGGPCAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 59  
 DB 1 MRRASRDYTKYLRSGEMGGPCAPHEGPHL-APPPAPHPAPPAASRSMFVALLGLGQ 60  
 QY 60 VVCSVALFFYFRAQMDPNRISDGTCHYIRLRLHENADFDQTTLESQDTKLIPDSCRRI 119  
 DB 61 VVCSIALFLYFRAQMDPNRISDGTCHYIRLRLHENAGLDSTLESDT--LPDSCRM 118  
 QY 120 KQAFQAVQKELQHVGSQHIRAEKAWDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 179  
 DB 119 KQAFQAVQKELQHVGSQHIRAEKAWDGSWLDLAKRSKLEAQPFAHLTINATDIPSGS 178  
 QY 180 HKVSLSSWYHDSGAWKISNNTFSGNKLIVNODGFYLYANICFRHHTSGDLATYQLQM 239  
 DB 179 HKVTLSSWYHDSGAWKISNNTFSGNKLIVNODGFYLYANICFRHHTSGDLATYQLQM 238  
 QY 240 VVYVTKTSIKIPSSHTLMKGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VVYVTKTSIKIPSSHTLMKGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 298  
 QY 300 DPQDATYFGAFKVRDID 317  
 DB 299 DPQDATYFGAFKVRDID 316

RESULT 11

AAW59654  
ID AAW59654 standard; Protein; 316 AA.

XX AC AAW59654;

XX DT 24-SEP-1998 (first entry)

XX DE Amino acid sequence of mouse 499E9 protein.

XX KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;  
XX KW antagonist; autoimmune disorder; rheumatoid arthritis;  
XX KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;  
XX KW acute inflammatory response; antibody; antigen; cancer.

XX OS 'Mus sp.'

XX FH Key Location/Qualifiers

XX ET Domain 1..49  
/note- "intracellular domain"  
Domain 70..316  
/note- "extracellular domain"

XX FN W09825958-A2.

XX PN 18-JUN-1998.

XX PD 12-DEC-1997; 97WO-US22766.

XX PF 13-DEC-1996; 96US-0032846.

XX PR (SCHE ) SCHERING CORP.

XX PA Gorman DM, Mattson JD;

XX PI WPI; 1998-348452/30.

XX DR N-PSDB; AAV41489.

XX PT Mouse cell surface antigen, 499E9 protein - used to treat conditions associated with abnormal physiology or development

XX PS Claim 1; Pages 8-11; 59pp; English.

XX CC This is the amino acid sequence of the mouse 499E9 protein, used in the method of the invention to treat conditions associated with abnormal physiology or development. The 499E9 protein is expressed highly on polarised Th1 T cells, binding of 499E9 to its receptor may result in either immune cell expansion or apoptosis. Antagonists of 499E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as acute inflammatory responses in which T-cell expansion, activation or immunological T-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful in detecting or diagnosing various immunological conditions related to the expression of antigens of 499E9. The antibodies, and fragments of 499E9 can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation (e.g. cancerous conditions) or degenerative conditions.

XX SQ Sequence 316 AA;

Query Match 84.1%; Score 1417.5; DB 19; Length 316;

Best Local Similarity 84.3%; Pred. No. 3.8e-130;

Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSEMGCGFAPHEGPHL-APPPHAPPPAASRSMFALLGLGQ 59

DB 1 MRRASRDYTKYLRSEMGCGFAPHEGPHL-APPPHAPPPAASRSMFALLGLGQ 60

QY 60 VVCSIALFFYFRAQMDPNRISEDTGTHCYIRILRHENADFDQTTLESQDTKLIPDCRR 119

DB 61 VVCSIALFFYFRAQMDPNRISEDTGTHCYIRILRHENAGLDSTLESDT--LPDSCRRM 118  
QY 120 KOAFQAVQKELQHVCSQHRAEKANVDCSWLDLAKRSKLEAOPFAHLTINATDIPSGS 179  
DB 119 KOAFQAVQKELQHVCSQHRAEKANVDCSWLDLAKRSKLEAOPFAHLTINATDIPSGS 178  
QY 180 HKVSLSSWYHDSRWAKISNMTFSGKLIIVNODGFYIYANICFRHHHETSGDLATFYL 239  
DB 179 HKVTLSSWYHDSRWAKISNMTFSGKLIIVNODGFYIYANICFRHHHETSGVPTDYQL 238  
QY 240 VYVTKTSIKIPSSHTLMKGGSTKYWNSSEFHYFYSINVGFFKLRSGEETISIEVSNP 299  
DB 239 VYVTKTSIKIPSSHTLMKGGSTKYWNSSEFHYFYSINVGFFKLRSGEETISIEVSNP 298  
QY 300 DPQDQATYFGAFKVRDID 317  
DB 299 DPQDQATYFGAFKVRDID 316

RESULT 12

AAV17874

ID AAV17874 standard; Protein; 316 AA.

XX AC AAV17874;

XX DT 17-AUG-1999 (first entry)

XX DE Murine TRANCE.

XX KW TRANCE: tumour necrosis factor superfamily; signal transduction; TNF;  
XX KW TNF-related activation induced cytokine; immune response; cancer;  
XX KW autoimmune disease; HIV; hypersensitivity; allergen.

XX OS Mus musculus.

XX PN W09929865-A2.

XX PD 17-JUN-1999.

XX PF 14-DEC-1998; 98WO-US26486.

XX PR 11-DEC-1998; 98US-0989479.

XX PR 12-DEC-1997; 97US-0989479.

XX PR 03-MAR-1998; 98US-0034099.

XX PA (UYRQ ) UNIV ROCKEFELLER.

XX PI Choi Y, Josien R, Steinman R, Won B;

XX DR WPI; 1999-385609/32.

XX DR N-PSDB; AAX80224.

XX PT TNF like proteins for treating autoimmunity and cancer

XX PS Claim 9; Fig 3; 164pp; English.

XX CC The present sequence represents murine TRANCE-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fragments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially CD40L or TNF-alpha).

XX SQ Sequence 316 AA;

Query Match 84.1%; Score 1417.5; DB 20; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSFVALLGLGLGQ 59  
 DB 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSFVALLGLGLGQ 60

QY 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFOPTTLESQTKLIPDSRR 119  
 DB 61 VVCSIALFLYFRAQMDPNRISEDGTHCIYRILRLHENADFOPTTLESQTKLIPDSRR 118

QY 120 KOAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHITINATIPSGS 179  
 DB 119 KOAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHITINATIPSGS 178

QY 180 HKVLSLSSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQ 239  
 DB 179 HKVLSLSSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQ 238

QY 240 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 298

QY 300 DPQDQATYFAGKVRDID 317  
 DB 299 DPQDQATYFAGKVRDID 316

RESULT 13  
 AAY91024  
 ID AAY91024 standard; Protein; 316 AA.  
 AC AAY91024;  
 DT 05-SEP-2000 (first entry)  
 DE Mouse OBM protein sequence SEQ ID NO:10.  
 KW Mouse; osteoclastogenesis inhibitory factor binding molecule; OCIF;  
 KW OBM; osteoclast; bone absorption promoting factor; vitamin D3; PTH;  
 KW parathyroid hormone.  
 XX Mus sp.  
 OS JP2000102390-A.  
 PD 11-APR-2000.  
 XX 30-SEP-1998; 98JP-0292971.  
 XX 30-SEP-1998; 98JP-0292971.  
 XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
 PA (YSNE-) YS NEW TECHNOLOGY KENKYUSHO.  
 XX WPI; 2000-332087/29.  
 DR N-PSDB; AAA39156.  
 XX A DNA and preparation of a protein by using it  
 PS Example 1; Page 15-16; 18pp; Japanese.  
 CC The present invention describes a genomic DNA encoding a protein having  
 an activity of supporting or promoting differentiation and maturation of  
 osteoclasts. The genomic DNA encoding a protein has the following  
 properties: (a) combines specifically with osteoclastogenesis inhibitory  
 factor (OCIF) and has a high affinity; (b) shows a molecular weight (mw)  
 of 30,000 to 40,000 by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide  
 gel electrophoresis) under a nonreductive condition and the apparent mw  
 when crosslinked with monomer type OCIF is 90,000 to 110,000; and (c)  
 has an activity of supporting or promoting differentiation and maturation

of osteoclast in the co-culture of mouse osteoblast-like stroma cell and  
 mouse spleen cell in the presence of a bone absorption promoting factor  
 such as active type vitamin D3 and parathyroid hormone (PTH). The protein  
 can be used as a drug and a research reagent. The present sequence  
 CC represents a mouse OCIF binding molecule (OBM) from the present  
 CC invention.

SQ Sequence 316 AA;

Query Match 84.1%; Score 1417.5; DB 21; Length 316;  
 Best Local Similarity 84.3%; Pred. No. 3.8e-130;  
 Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSFVALLGLGLGQ 59  
 DB 1 MRRASRDYTKYLRSEEMGGGPGAPHEGLH-APPPAPHPAPPAASRSFVALLGLGLGQ 60

QY 60 VVCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFOPTTLESQTKLIPDSRR 119  
 DB 61 VVCSIALFLYFRAQMDPNRISEDGTHCIYRILRLHENADFOPTTLESQTKLIPDSRR 118

QY 120 KOAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHITINATIPSGS 179  
 DB 119 KOAFQAGVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHITINATIPSGS 178

QY 180 HKVLSLSSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQ 239  
 DB 179 HKVLSLSSWYHDSRWAKISNMTFSNGKLIYNQDGFYLYANICFRHHETSGDLATEYLQ 238

QY 240 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299  
 DB 239 VYVTKTSIKIPSSHTLMKGGSTKNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 298

QY 300 DPQDQATYFAGKVRDID 317  
 DB 299 DPQDQATYFAGKVRDID 316

RESULT 14  
 AAY84418  
 ID AAY84418 standard; Protein; 316 AA.  
 AC AAY84418;  
 DT 25-JUL-2000 (first entry)  
 DE Amino acid sequence of a murine osteoprotegerin ligand (OPGL).  
 KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;  
 KW tumour necrosis factor receptor; type II transmembrane protein;  
 KW osteoclast differentiation; CSF-1; osteoclast activator;  
 KW immune response; osteoporosis; bone resorption.  
 XX Mus musculus.  
 OS  
 EH Key  
 FT Domain  
 FT 48..71  
 FT /note= "transmembrane domain"  
 FT 70..157  
 FT /note= "extracellular stalk domain"  
 FT 152..316  
 FT /note= "tumour necrosis factor-like domain"  
 FT 158..317  
 FT /note= "active ligand moiety"  
 XX WO200015807-A1.  
 XX 23-MAR-2000.  
 XX 13-SEP-1999; 99WO-DK00481.  
 XX 15-SEP-1998; 98DK-0001164.  
 PR 02-OCT-1998; 98US-0102896.

```

XX PA (MEBI-) M & E BIOTECH AS.
XX PI Halkier T, Haaning J;
XX DR WPI; 2000-271444/23.
XX DR N-PSDB; AA299965.
XX XX
XX PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX FT to treat, prevent and ameliorate osteoporosis -
XX PS Claim 17; Page 81-82; 110pp; English.
XX CC
XX CC The present sequence represents a murine osteoprotegerin ligand (OPGL).
XX CC Osteoprotegerin is a secreted member of the tumour necrosis factor
XX CC receptor family, which blocks osteoclastogenesis in a dose dependent
XX CC manner. The OPGL protein is synthesised as a type II transmembrane
XX CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
XX CC is a potent osteoclast differentiation factor when combined with CSF-1.
XX CC It is not capable of inducing osteoclast differentiation in the absence
XX CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
XX CC specification describes a method for the in vivo down-regulation of
XX CC OPGL activity in an animal. The method comprises using at least one OPGL
XX CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
XX CC an immune response in the animal. The method and OPGL polypeptide are
XX CC useful for treating, preventing and ameliorating osteoporosis or other
XX CC diseases or conditions characterised by excessive bone resorption.
XX SQ Sequence 316 AA;
XX CC
XX CC Query Match 84.1%; Score 1417.5; DB 21; Length 316;
XX CC Best Local Similarity 84.3%; Pred. No. 3.8e-130;
XX CC Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;
XX CC
QY 1 MRRASRDYTKYLRSEEMGGPGAPHEGLH-APPPHAPPAPPAASRSMFVALLGLGLGQ 59
DB 1 MRRASRDYTKYLRSEEMGGPGVPHEGLHAPAPAPAPPAASRSMFVALLGLGLGQ 60
QY 60 VVCSVALFFYFRAQMDPNRISEDCGTHCYIRLRLHENADFODTTLESODTKLIPDSCRR 119
DB 61 VVCSIALFLYFRAQMDPNRISEDCGTHCYIRLRLHENAGLDSTLESDT--LPDSCRRM 118
QY 120 KQAFQAVQKELQHVGSQHTRAEKAMVDGSLDLAKRSKLEAQPFAHLLTNATDIPSGS 179
DB 119 KQAFQAVQKELQHVGPQFSGAPAMMEGSLDVAQKPEAQPFAHLLTNAAIPSGS 178
QY 180 HKVLSLSSWYHDRGWAKISNMTFFSNGKLIVNODGGFYLYANICFRHHETSGVPTDYQLM 239
DB 179 HKVTLSSWYHDRGWAKISNMTLSNGLKRVNODGGFYLYANICFRHHETSGVPTDYQLM 238
QY 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSSEPHFYSINVGFFKLRSRGEISIEVSNPSSL 299
DB 239 VYVTKTSIKIPSSHNLKMGSTKNWSGNSSEPHFYSINVGFFKLRSRGEISIEVSNPSSL 298
XX CC
XX CC RESULT 15
XX CC ID AAY84419
XX CC AC AAY84419 standard; Protein; 316 AA.
XX CC
XX CC 25-JUL-2000 (first entry)
XX CC
XX CC Amino acid sequence of a murine osteoprotegerin ligand (OPGL).
XX CC
XX CC Osteoprotegerin ligand: OPGL; osteoprotegerin; osteoclastogenesis;
XX CC tumour necrosis factor receptor; type II transmembrane protein;
XX CC osteoclast differentiation; CSF-1; osteoclast activator;
XX CC immune response; osteoporosis; bone resorption.

```

```

XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT Region 49..69 /note= "transmembrane region"
XX FT Domain 70..157 /note= "extracellular stalk domain"
XX FT Region 158..317 /note= "active ligand moiety"
XX XX
XX PN W0200015807-A1.
XX XX
XX PD 23-MAR-2000.
XX XX
XX PF 13-SEP-1999; 99WO-DK00481.
XX XX
XX PR 15-SEP-1998; 98DK-0001164.
XX PR 02-OCT-1998; 98US-0102896.
XX XX
XX PA (MEBI-) M & E BIOTECH AS.
XX XX
XX PI Halkier T, Haaning J;
XX DR WPI; 2000-271444/23.
XX DR N-PSDB; AA299966.
XX XX
XX PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX FT to treat, prevent and ameliorate osteoporosis -
XX PS Claim 17; Page 85-86; 110pp; English.
XX CC
XX CC The present sequence represents a murine osteoprotegerin ligand (OPGL).
XX CC Osteoprotegerin is a secreted member of the tumour necrosis factor
XX CC receptor family, which blocks osteoclastogenesis in a dose dependent
XX CC manner. The OPGL protein is synthesised as a type II transmembrane
XX CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
XX CC is a potent osteoclast differentiation factor when combined with CSF-1.
XX CC It is not capable of inducing osteoclast differentiation in the absence
XX CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
XX CC specification describes a method for the in vivo down-regulation of
XX CC OPGL activity in an animal. The method comprises using at least one OPGL
XX CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
XX CC an immune response in the animal. The method and OPGL polypeptide are
XX CC useful for treating, preventing and ameliorating osteoporosis or other
XX CC diseases or conditions characterised by excessive bone resorption.
XX SQ Sequence 316 AA;
XX CC
XX CC Query Match 84.1%; Score 1417.5; DB 21; Length 316;
XX CC Best Local Similarity 84.3%; Pred. No. 3.8e-130;
XX CC Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;
XX CC
QY 1 MRRASRDYTKYLRSEEMGGPGAPHEGLH-APPPHAPPAPPAASRSMFVALLGLGLGQ 59
DB 1 MRRASRDYTKYLRSEEMGGPGVPHEGLHAPAPAPAPPAASRSMFVALLGLGLGQ 60
QY 60 VVCSVALFFYFRAQMDPNRISEDCGTHCYIRLRLHENADFODTTLESODTKLIPDSCRR 119
DB 61 VVCSIALFLYFRAQMDPNRISEDCGTHCYIRLRLHENAGLDSTLESDT--LPDSCRRM 118
QY 120 KQAFQAVQKELQHVGSQHTRAEKAMVDGSLDLAKRSKLEAQPFAHLLTNATDIPSGS 179
DB 119 KQAFQAVQKELQHVGPQFSGAPAMMEGSLDVAQKPEAQPFAHLLTNAAIPSGS 178
QY 180 HKVLSLSSWYHDRGWAKISNMTFFSNGKLIVNODGGFYLYANICFRHHETSGVPTDYQLM 239
DB 179 HKVTLSSWYHDRGWAKISNMTLSNGLKRVNODGGFYLYANICFRHHETSGVPTDYQLM 238
QY 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSSEPHFYSINVGFFKLRSRGEISIEVSNPSSL 299
DB 239 VYVTKTSIKIPSSHNLKMGSTKNWSGNSSEPHFYSINVGFFKLRSRGEISIEVSNPSSL 298

```

Qy 300 DPQDATYFGAFKVRDID 317  
|||||  
Db 299 DPQDATYFGAFKVRDID 316

Search completed: October 10, 2002, 16:00:55  
Job time : 88.9789 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 37.2379 seconds  
(without alignments)  
329.613 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRYTKYLRGSEEMGG.....LLDPDQDATYGFQKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Arched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Match | Length | ID          | Description         |
|------------|--------|-------|--------|-------------|---------------------|
| 1          | 1685   | 100.0 | 317    | TN11_HUMAN  | O14788 h tumor nec  |
| 2          | 1417.5 | 84.1  | 316    | TN11_MOUSE  | O35235 m tumor nec  |
| 3          | 251.5  | 14.9  | 281    | TN10_HUMAN  | P50591 homo sapien  |
| 4          | 248    | 14.7  | 291    | TN10_MOUSE  | P50592 mus musculu  |
| 5          | 189    | 11.2  | 281    | TN10_HUMAN  | P48023 homo sapien  |
| 6          | 184.5  | 10.9  | 279    | FASL_MOUSE  | P41047 mus musculu  |
| 7          | 176.5  | 10.5  | 261    | TN10_BOVIN  | P51749 bos taurus   |
| 8          | 175.5  | 10.4  | 278    | FASL_RAT    | P36940 rattus norv  |
| 9          | 158.5  | 9.4   | 261    | TN10_HUMAN  | P29965 homo sapien  |
| 10         | 152    | 9.0   | 260    | TN10_FELCA  | O97605 felis silve  |
| 11         | 146    | 8.7   | 234    | TN10_CANVPO | P51435 canis porce  |
| 12         | 145    | 8.6   | 260    | TN10_CANFA  | O97626 canis famill |
| 13         | 141.5  | 8.4   | 235    | TN10_MOUSE  | P06804 mus musculu  |
| 14         | 140.5  | 8.3   | 235    | TN10_RABIT  | P04924 oryctolagus  |
| 15         | 137    | 8.1   | 234    | TN10_SHEEP  | P23383 ovis aries   |
| 16         | 134    | 8.0   | 233    | TN10_MACFA  | P79337 macaca fasc  |
| 17         | 134    | 8.0   | 240    | TN10_HUMAN  | O43557 homo sapien  |
| 18         | 133    | 7.9   | 233    | TN10_CANFA  | P51742 canis famill |
| 19         | 133    | 7.9   | 233    | TN10_HUMAN  | P01375 homo sapien  |
| 20         | 133    | 7.9   | 233    | TN10_MACMU  | P48094 macaca mula  |
| 21         | 132.5  | 7.9   | 235    | TN10_PERLE  | P36939 peromyscus   |
| 22         | 131.5  | 7.8   | 235    | TN10_RAT    | P16599 rattus norv  |
| 23         | 130.5  | 7.7   | 306    | TN10_MOUSE  | P41155 mus musculu  |
| 24         | 130    | 7.7   | 233    | TN10_PAPSP  | P33620 papio sp. (  |
| 25         | 129.5  | 7.7   | 233    | TN10_MARMO  | O35734 marmota mon  |
| 26         | 129    | 7.7   | 233    | TN10_PAPHU  | O77510 papio hamad  |
| 27         | 128    | 7.6   | 234    | TN10_HORSE  | P29553 equus cabal  |
| 28         | 126.5  | 7.5   | 233    | TN10_BOVIN  | O06599 bos taurus   |
| 29         | 126    | 7.5   | 232    | TN10_PIG    | P23563 sus scrofa   |
| 30         | 122    | 7.2   | 193    | TN10_CAPHI  | P13296 capra hircu  |
| 31         | 120    | 7.1   | 229    | TN10_CEREL  | P51743 cervus elap  |
| 32         | 118    | 7.0   | 260    | TN10_MOUSE  | P27548 mus musculu  |
| 33         | 117    | 6.9   | 233    | TN10_FELCA  | P19101 felis silve  |

|    |      |     |      |   |            |                     |
|----|------|-----|------|---|------------|---------------------|
| 34 | 117  | 6.9 | 244  | 1 | TNFC_HUMAN | Q05643 homo sapien  |
| 35 | 116  | 6.9 | 233  | 1 | TNFA_WACEU | O77764 macropus eu  |
| 36 | 105  | 6.2 | 201  | 1 | TNFB_WACEU | Q9448 macropus eu   |
| 37 | 97   | 5.8 | 1464 | 1 | CALL_HUMAN | P02452 homo sapien  |
| 38 | 95   | 5.6 | 858  | 1 | V2A_CAVK   | Q86783 cucumber mo  |
| 39 | 93   | 5.5 | 233  | 1 | TNFA_TRIYU | P79374 trichosurus  |
| 40 | 92.5 | 5.5 | 205  | 1 | TNFB_HUMAN | P01374 homo sapien  |
| 41 | 92.5 | 5.5 | 450  | 1 | YK22_YEAST | P36135 saccharomyc  |
| 42 | 92   | 5.5 | 857  | 1 | V2A_CAVNT  | O40977 cucumber mo  |
| 43 | 90.5 | 5.4 | 858  | 1 | V2A_CAVAS  | Q39436 cucumber mo  |
| 44 | 90.5 | 5.4 | 1694 | 1 | SN_MOUSE   | Q62230 mus musculu  |
| 45 | 90   | 5.3 | 1460 | 1 | CALL_CANFA | Q9x5j7 canis famill |

## ALIGNMENTS

|            |  |           |      |     |     |  |
|------------|--|-----------|------|-----|-----|--|
| RESULT 1   |  |           |      |     |     |  |
| TN11_HUMAN |  |           |      |     |     |  |
| ID         | TN11_HUMAN   | STANDARD; | PRT; | 317 | AA. |  |
| AC         | O14788: O14723; Q9P203;  |           |      |     |     |  |
| DT         | 16-OCT-2001 (Rel. 40, Created)   |           |      |     |     |  |
| DT         | 16-OCT-2001 (Rel. 40, Last sequence update)                            |           |      |     |     |  |
| DE         | Tumor necrosis factor ligand superfamily member 11 (Receptor activator |           |      |     |     |  |
| DE         | of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-     |           |      |     |     |  |
| DE         | induced cytokine) (TNF) (Osteoprotegerin ligand) (OPGL) (Osteoclast    |           |      |     |     |  |
| DE         | differentiation factor) (ODF) (ODF).                                   |           |      |     |     |  |
| GN         | TNFSF11 OR RANKL OR TNF OR OPGL.                                       |           |      |     |     |  |
| OS         | Homo sapiens (Human).  |           |      |     |     |  |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |           |      |     |     |  |
| OC         | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.             |           |      |     |     |  |
| OX         | NCBI_TaxID:9606;   |           |      |     |     |  |
| RN         | [1]  |           |      |     |     |  |
| RP         | SEQUENCE FROM N.A.   |           |      |     |     |  |
| RC         | TISSUE-Bone marrow, and Peripheral blood;                              |           |      |     |     |  |
| RX         | MEDLINE-98032977; PubMed-9367155;                                      |           |      |     |     |  |
| RA         | Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,         |           |      |     |     |  |
| RA         | Tcmetsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,          |           |      |     |     |  |
| RA         | Galibert L.,   |           |      |     |     |  |
| RT         | "A homologue of the TNF receptor and its ligand enhance T-cell growth  |           |      |     |     |  |
| RT         | and dendritic-cell function."  |           |      |     |     |  |
| RL         | Nature 390:175-179(1997).  |           |      |     |     |  |
| RN         | [2]  |           |      |     |     |  |
| RP         | SEQUENCE FROM N.A.   |           |      |     |     |  |
| RC         | TISSUE-Lymph node;   |           |      |     |     |  |
| RC         | MEDLINE-9827661; PubMed-9568710;                                       |           |      |     |     |  |
| RA         | Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,            |           |      |     |     |  |
| RA         | Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,   |           |      |     |     |  |
| RA         | Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,   |           |      |     |     |  |
| RA         | Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Delaney J.,            |           |      |     |     |  |
| RA         | Boyle W.J.,  |           |      |     |     |  |
| RT         | "Osteoprotegerin ligand is a cytokine that regulates osteoclast        |           |      |     |     |  |
| RT         | differentiation and activation."                                       |           |      |     |     |  |
| RL         | Cell 93:165-176(1998).   |           |      |     |     |  |
| RN         | [3]  |           |      |     |     |  |
| RP         | SEQUENCE OF 73-317 FROM N.A.   |           |      |     |     |  |
| RC         | TISSUE-Thymocytes;   |           |      |     |     |  |
| RC         | MEDLINE-97460112; PubMed-9312132;                                      |           |      |     |     |  |
| RA         | Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,        |           |      |     |     |  |
| RA         | Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,   |           |      |     |     |  |
| RA         | Choi Y.,   |           |      |     |     |  |
| RT         | "TNF is a novel ligand of the tumor necrosis factor receptor family    |           |      |     |     |  |
| RT         | that activates c-Jun N-terminal kinase in T cells."                    |           |      |     |     |  |
| RL         | J. Biol. Chem. 272:25190-25194(1997).                                  |           |      |     |     |  |
| RN         | [4]  |           |      |     |     |  |
| RP         | SEQUENCE FROM N.A. (ISOFORM 2).  |           |      |     |     |  |
| RC         | TISSUE-Tongue;   |           |      |     |     |  |
| RC         | MEDLINE-20175237; PubMed-10708588;                                     |           |      |     |     |  |
| RA         | Nagai M., Kyakumoto S., Sato N.,                                       |           |      |     |     |  |
| RT         | "Cancer cells responsible for humoral hypercalcemia express mRNA       |           |      |     |     |  |
| RT         | encoding a secreted form of ODF/TNFR that induces osteoclast           |           |      |     |     |  |
| RT         | formation."  |           |      |     |     |  |



Biochem. Biophys. Res. Commun. 269:532-536(2000).

-1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.

AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE. MAY ALSO PLAY AN IMPORTANT ROLE IN ENHANCED BONE-RESORPTION IN HUMORAL HYPERCALCAEMIA OF MALIGNANCY.

-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (ISOFORM 1) AND SECRETED (ISOFORM 2).

-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2/SODF; ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART, PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.

-1- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; AF019047; AAB86811.1; -

EMBL; AF053712; AAC39731.1; -

EMBL; AF013171; AAC51762.1; -

EMBL; AB037599; BAA90488.1; -

MIM; 602642; -

InterPro: IPR003263; TNF\_5.

InterPro: IPR000478; TNF\_family.

Pfam: PF00229; TNF; 1.

ProDom: PD008600; TNF\_5; 1.

SMART; SM00207; TNF; 1.

PROSITE; PS00251; TNF\_1; FALSE\_NEG.

PROSITE; PS00049; TNF\_2; 1.

Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Alternative splicing.

DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).

TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).

DOMAIN 69 317 EXTRACELLULAR (POTENTIAL).

CARBOHYD 171 171 N-LINKED (GLCNAC... ) (POTENTIAL).

CARBOHYD 198 198 N-LINKED (GLCNAC... ) (POTENTIAL).

VARSPLIC 1 73 MISSING (IN ISOFORM 2).

CONFLICT 194 194 A -> G (IN REF. 3).

SEQUENCE 317 AA; 35478 MW; 766176446348097f CRC64;

Query Match 100.0%; Score 1685; DB 1; Length 317;

Best Local Similarity 100.0%; Pred. No. 7.4e-136;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRASRDYTKYLRSEMGSGGPHGPHLHAPPHPAPPAPPAASRSMFVALLGLGLGV 60

DB 1 MRRASRDYTKYLRSEMGSGGPHGPHLHAPPHPAPPAPPAASRSMFVALLGLGLGV 60

QY 61 VCSVALFFYFRAQDMPNRISDGTGTCYRILRLHENADFQTTLESQDTKLIPDSCKRIK 120

DB 61 VCSVALFFYFRAQDMPNRISDGTGTCYRILRLHENADFQTTLESQDTKLIPDSCKRIK 120

QY 121 QAFQVQKELQHVGSQIHIAEKAVDQSWLDLAKRSKLEAQPFAHLLTINATDIPSGSH 180

DB 121 QAFQVQKELQHVGSQIHIAEKAVDQSWLDLAKRSKLEAQPFAHLLTINATDIPSGSH 180

QY 181 KVSLSWYHDSGAKISNMTFSNGLIYNQDFFYLYANICFRHETSGDLATEYLQLMV 240

DB 181 KVSLSWYHDSGAKISNMTFSNGLIYNQDFFYLYANICFRHETSGDLATEYLQLMV 240

QY 241 YVTKTSIKIPSSHTLMKGGSTKYSGNSEFHYFYSINVGGFYKLRSGEISIEVSNPSLID 300

DB 241 YVTKTSIKIPSSHTLMKGGSTKYSGNSEFHYFYSINVGGFYKLRSGEISIEVSNPSLID 300

QY 301 PPDATYGAFAKVRDID 317

DB 301 PPDATYGAFAKVRDID 317

RESULT 2

TNII\_MOUSE

ID TNII\_MOUSE STANDARD; PRT; 316 AA.

AC O35235; O35305;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF) (Osteoclastogenesis-inhibitory factor) (OCIF).

GN TNFSF11 OR RANKL OR TRANCE OR OPGL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Hybridoma;

RX MEDLINE-97460112; PubMed-9312132;

RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y., Choi Y.;

RA "TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";

RL J. Biol. Chem. 272:25190-25194(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE-Bone marrow;

RX MEDLINE-98227661; PubMed-9568710;

RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;

RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.";

RL Cell 93:165-176(1998).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE-Bone marrow stroma;

RX MEDLINE-98188248; PubMed-9520411;

RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M., Tsuda E., Mochizuki S.-I., Tomoyasu A., Yanai K., Goto M., Murakami A., Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;

RA "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE-Thymic lymphoma;

RX MEDLINE-98032977; PubMed-9367155;

RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubs R.F., Cosman D., Galibert L.;

RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";

RL Nature 390:175-179(1997).

RN [5]

RP SEQUENCE FROM N.A.

RC Ikeda T.;

RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR. AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL PROLIFERATION. MAY BE AN IMPORTANT REGULATOR OF INTERACTIONS

CC BETWEEN T CELLS AND DENDRITIC CELLS AND MAY PLAY A ROLE IN THE  
CC REGULATION OF THE T CELL-DEPENDENT IMMUNE RESPONSE.  
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (potential).  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT  
CC NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS  
CC BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE  
CC TRABECULAR BONE AND LUNG.  
CC -1- DISEASE: DEFICIENCY IN TNFSF11 RESULTS IN FAILURE TO FORM LOBULO-  
CC ALVEOLAR MAMMARY STRUCTURES DURING PREGNANCY, RESULTING IN DEATH  
CC OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH  
CC NO OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT  
CC PROFOUND GROWTH RETARDATION AT SEVERAL SKELETAL SITES, INCLUDING  
CC THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA,  
CC WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN  
CC HYPERTROPHIC CHONDROCYTES.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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CC  
CC EMBL; AF053713; AAC40113.1; -  
CC EMBL; AF013170; AAC71061.1; -  
CC EMBL; AB008426; BAA25425.1; -  
CC EMBL; AF019048; AAB86812.1; -  
CC EMBL; AB036798; BAA97259.1; -  
CC MGD; MGI:1100089; Tnfesf11.  
CC InterPro; IPR003263; TNF-5.  
CC InterPro; IPR000478; TNF\_family.  
CC Pfam; PF00229; TNF; 1.  
CC ProDom; PD008600; TNF\_5; 1.  
CC SMART; SM00207; TNF; 1.  
CC PROSITE; PS00251; TNF\_1; FALSE\_NEG.  
CC PROSITE; PS00049; TNF\_2; 1.  
CC Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;  
CC Signal-anchor.  
CC DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).  
CC TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)  
CC (POTENTIAL).  
CC DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).  
CC CARBOHYD 197 197 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CARBOHYD 262 262 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CONFLICT 99 99 G -> D (IN REF. 4).  
CC SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;  
Query Match 84.1%; Score 1417.5; DB 1; Length 316;  
Best Local Similarity 84.3%; Pred. No. 3.9e-113;  
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;  
QY 1 MRRASRDYTYLRSSEMGPGAPHEGPHL-APPPAPAPHPAPPAASRMFVALIGLIGLQ 59  
DB 1 MRRASRDYTYLRSSEMGPGAPHEGPHLAPAPAPAPPAASRMFVALIGLIGLQ 60  
QY 60 VVCSVALFFYFRAQMDPNRISEDTGTHCIYILRLHFNADFTDLESODTKLIPDSCHRI 119  
DB 61 VVCSIALFLYFRAQMDPNRISEDTGTHCIYILRLHFNADFTDLESODTKLIPDSCHRI 118  
QY 120 KQAFQAVQKELHIVGSOHRAEKAMVDGSLDLAKSKLEAOPFAHLTINATDIPSGS 179  
DB 119 KQAFQAVQKELHIVGSOHRAEKAMVDGSLDLAKSKLEAOPFAHLTINATDIPSGS 178  
QY 180 HKVLSLSWYHDSRWAKISNTTFSNGKLIVNGDGYLYLYANICFRHHTSGDLATEYQLQM 239  
DB 179 HKVLSLSWYHDSRWAKISNTTFSNGKLIVNGDGYLYLYANICFRHHTSGDLATEYQLQM 238  
QY 240 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEPHFYSINVGGFKLRSGEISIEVSNPSLL 299  
DB 239 VYVTKTSIKIPSSHTLMKGGSTKYWSGNSEPHFYSINVGGFKLRSGEISIEVSNPSLL 298

QY 300 DPQDQATYFGAFKVRDID 317  
DB 299 DPQDQATYFGAFKVRDID 316  
RESULT 3  
TN10\_HUMAN STANDARD; PRT; 281 AA.  
ID TN10\_HUMAN STANDARD; PRT; 281 AA.  
AC P50591;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor ligand superfamily member 10 (TNF-related  
DE apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).  
GN TNFSF10 OR TRAIL OR APO2L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96111955; PubMed=8777713;  
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,  
RA Goodwin R.G.;  
RT "Identification and characterization of a new member of the TNF  
RT family that induces apoptosis."  
RL Immunity 3:673-682(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE-Placenta;  
RX MEDLINE=96278649; PubMed=8663110;  
RA Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,  
RA Ashkenazi A.;  
RT "Induction of apoptosis by Apo-2 ligand, a new member of the tumor  
RT necrosis factor cytokine family."  
RL J. Biol. Chem. 271:12687-12690(1996).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.  
RX MEDLINE=20017054; PubMed=10549288;  
RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,  
RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
RT complex with death receptor 5."  
RL Mol. Cell 4:563-571(1999).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.  
RX PubMed=10542098;  
RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
RA Jones E.Y., Srean G.R.;  
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
RT specificity in apoptotic initiation."  
RL Nat. Struct. Biol. 6:1048-1053(1999).  
CC -1- FUNCTION: INDUCES APOPTOSIS.  
CC -1- SUBUNIT: HOMOTRIMER (POTENTIAL).  
CC -1- SUBCELLULAR LOCATION: TYPE II membrane protein (Potential).  
CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG  
CC AND PROSTATE.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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CC  
CC EMBL; U37518; AAC50332.1; -  
CC EMBL; U57059; AAB01233.1; -  
CC MIM; 603598; -  
CC PDB; 1D0G; 22-OCT-99.  
CC PDB; 1D4V; 01-NOV-99.

[illegible]

RA MEDLINE-95127560; PubMed-7826947;  
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;  
RT "Human Fas ligand: gene structure, chromosomal location and species  
RT specificity.";  
RL Int. Immunol. 6:1567-1574(1994).  
RN [3]  
RN SEQUENCE FROM N.A.  
RP Schaeuble C.E., Pohlmann R., Philippson P., Eibel H.;  
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
RL [4]  
RN SEQUENCE FROM N.A.  
RX MEDLINE-95071350; PubMed-7980502;  
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,  
RA Fusamoto H., Kamada T.;  
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus  
RT infection.";  
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).  
RN [5]  
RN SEQUENCE FROM N.A.  
RP Wilkinson J.;  
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RL [6]  
RN SEQUENCE OF 1-10 FROM N.A.  
RC TISSUE-Blood;  
RA Matsumura M., Nakanishi Y., Ohba Y.;  
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN. A RECEPTOR THAT  
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
CC T CELLS, OR BOTH.  
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).  
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED  
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL  
CC SURFACE.  
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC -!- DATABASE: NAME-PRO; NOTE-CD guide CD178 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/3338769674\_g.htm".  
CC -----  
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CC -----  
DR EMBL; X89102; CAA61474.1; -  
DR EMBL; U08137; AAC50071.1; -  
DR EMBL; U11821; AAC50124.1; -  
DR EMBL; D38122; BAA07320.1; -  
DR EMBL; Z96050; CAB09424.1; -  
DR EMBL; AB013303; BAA32542.1; -  
DR HSP; P06804; 2TNE.  
DR MIM; 134638; -  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_abc; 1.  
DR ProDom; PD008600; TNF\_5; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS00049; TNF\_2; 1.  
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;  
KW Antigen.  
FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).  
FT PRO-RICH 4 70  
FT DOMAIN 45 65 POLY-PRO.  
FT DISULFID 202 233 BY SIMILARITY.

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 281 AA; 31485 MW; ABA6EB358246E9BB CRC64;  
Query Match. 11.2%; Score 189; DB 1; Length 281;  
Best Local Similarity 21.7%; Pred. No. 7.6e-09;  
Matches 69; Conservative 43; Mismatches 98; Indels 10; Gaps 11;  
QY 22 PGAPHEGSLHAPPPAP-----HOPPAASRS-----MFVALGILGLGVVCS 63  
DB 46 PPP 100  
QY 64 VALFFYFRAQMDPNRISDGTCHCIYRILRLHENADQDTTLESODTKLIPDSCRRKQAF 123  
DB 101 --MFQLFHLQ-----KELAELESTSMHTA-----124  
QY 124 QGAVQKELHIVGSHIRAEKAMVDGSLDLAKRSKLEAQFAHLT--INATDIPSGSHK 181  
DB 125 --SSLEKQIGH-----PSPPEKKEKVAHLTKGKSNRSM-----159  
QY 182 VSLSSVYHGRGKAKISNMTFSNGLKLVNODGFYLVANICFRHNETSGDLATEYLQLMVY 241  
DB 160 ---LEWEDTYGIVLLSGVYKKGGLVINEYGLYFVSKYVFRGQSCNN-----LPLSHK 210  
QY 242 VTKTSIKIPSSHTIMKGGSTKY-----WSGNSSEHFYSINVGFFKLRSGEEISIEVSN 295  
DB 211 VYMRNSKYPDLYNMEGKMMSYCTTGOMWARS-----YLGAVPNLTSADHLVNVSE 263  
QY 296 PSLLDPDQDATYGAFAV 313  
DB 264 LSLVNFESQTFGLYKL 281  
RESULT 6  
FASL\_MOUSE STANDARD; PRT; 279 AA.  
AC P41047; Q61217; Q9R1F2;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE FAS antigen ligand.  
GN TNFSF6 OR APT1L1 OR FASL OR GLD.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE-94185175; PubMed-7511063;  
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,  
RA Suda T., Nagata S.;  
RT "Generalized lymphoproliferative disease in mice, caused by a point  
RT mutation in the Fas ligand.";  
RL Cell 76:969-976(1994).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.  
RC STRAIN=C57BL/6;  
RX MEDLINE-95388076; PubMed-7544870;  
RA Peitsch M.J., Tschoep J.J.;  
RT "Comparative molecular modelling of the Fas-ligand and other members  
RT of the TNF family.";  
RL Mol. Immunol. 32:761-772(1995).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).  
RX MEDLINE-95196085; PubMed-7889405;  
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a  
RT TNF family gene cluster.";  
RL Immunity 1:131-136(1994).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM FASL).

RC STRAIN-BALB/C;  
RA Penner M.H., Shioda T., Isselbacher K.J.;  
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in  
FT two amino acids."  
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM FASLS).  
RC STRAIN-C3H; TISSUE-Spleen;  
RX MEDLINE-20021694; PubMed-10552956;  
RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,  
RA Cannarile L., Migliorati G., Defino D.V., Riccardi C.;  
RT "Cloning and expression of a short Fas ligand: A new alternatively  
FT spliced product of the mouse Fas ligand gene."  
RL Blood 94:3456-3467(1999).  
RN [6]  
RP CHARACTERIZATION OF VARIANT GLD.  
RX MEDLINE-96091792; PubMed-7495745;  
RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,  
RA Rousseau M., Bron C., Renno T., French L., Tschoep J.;  
RT "Characterization of the non-functional Fas ligand of gld mice."  
FT Int. Immunol. 7:1381-1386(1995).  
RC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
FT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
RT CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
CC T CELLS, OR BOTH.  
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).  
CC -1- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.  
CC ISOFORM FASLS IS SOLUBLE.  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS  
CC WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL  
CC INTERACTION.  
CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED  
CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE  
CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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CC  
CC EMBL; U06948; AAA17800.1;  
DR EMBL; U10984; AAA19778.1;  
DR EMBL; S76752; AAB33780.1;  
DR EMBL; U58995; AAB02915.1;  
DR EMBL; AF119335; AAD52106.1;  
DR HSSP; P01375; 4TSV.  
DR MGD; MGI:99255; Tnfrsf6.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR003636; TNF abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD002012; TNF\_abc; 1.  
DR ProDom; PD008600; TNF\_5; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF 1; 1.  
DR PROSITE; PS0049; TNF 2; 1.  
DR Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;  
KW Disease mutation; Alternative splicing.  
FT DOMAIN 1 78  
FT SIGNAL-ANCHOR (POTENTIAL).  
FT TRANSMEM 79 100  
FT DOMAIN 101 279  
FT PRO-RICH.  
FT DOMAIN 4 69  
FT POLY-PRO.  
FT DOMAIN 45 51  
FT DISULFID 200 231  
FT CARBOHYD 117 117  
FT N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 182 182

FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 1 210 MISSING (IN ISOFORM FASLS).  
FT VARIANT 184 184 T -> A (IN STRAIN BALB/C).  
FT VARIANT 218 218 E -> G (IN STRAIN BALB/C).  
FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL  
FT TO ITS RECEPTOR).  
SQ SEQUENCE 279 AA; 31442 MW; 37972728E0A1CA CRC64;  
Query Match 10.9% Score 184.5; DB 1; Length 279;  
Best Local Similarity 21.7%; Pred No. 1.8e-08;  
Matches 70; Conservative 45; Mismatches 106; Indels 101; Gaps 11;  
QY 13 RGSEMGCGGAPHEGLHAPPPHAPHOP-----PAASRSMFVALLGLGL 57  
DB 38 RGPDRRPPPPPPVSPPLPPSPQLPLPLPLPLPLPLPLPLPLPLPLPLPL 97  
QY 58 GOVCSVALFFYFRAQMDPNRISEGDTHCIYRILRLHENADFQDTLESQDTKLIPDSR 117  
DB 98 G-----MYQLFHL----- 105  
QY 118 RIKQAFQAVOKLOHI--VGSQHRA--EKAMVDGSMWLDLAKRSKLEAQPFAHLTINA 172  
DB 106 -----OKELAELEFETNQSLKVSFKEQIANPS-----TPSEKKEPRVAHLTGN- 150  
QY 173 TDIPSGSHKVSLS-SWYHNRGWAKISNMTFSNGKLIVNQDGFYIYLYANICFRHETSGDL 231  
DB 151 -----PHSRISPLEMEDTYGTALISGVKKYKGLVINETGLYFYVYVFRGQSCN--- 201  
QY 232 ATEYLQLMVYVTKTSIKIPSSHTLMKGGSTKYWSNSENSEHFYSINVGFFKLRSGEIS 291  
DB 202 -NOPLNHHKVMYRNS--KYPEDLVLMEEKRLNYCT-TGQIWAHSSYLGAVENTLSADHLVY 257  
QY 292 EYSNPSLLDPDODATYFGAFKV 313  
DB 258 NISQSLNFEESKTFYGLYKL 279  
RESULT 7  
TNF5\_BOVIN  
ID TNF5\_BOVIN STANDARD; PRT; 261 AA.  
AC P51749;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CD40 ligand (TNF-related activation protein) (TRAP) (T cell antigen  
DE GP39).  
GN TNF5 OR CD40LG OR CD40L.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Blood;  
RX MEDLINE-96006582; PubMed-7590981;  
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;  
RT "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand  
RT and tumor necrosis factor alpha."  
RL Immunogenetics 42:430-431(1995).  
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-  
CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.  
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC  
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CC EMBL; 248469; CA88363.1; -  
 CC HSSP; P29965; IALY.  
 CC InterPro; IPR003263; TNF\_5.  
 CC InterPro; IPR000478; TNF\_family.  
 CC Pfam; PF00229; TNF; 1.  
 CC ProDom; PD008600; TNF\_5; 1.  
 CC SMART; SM00207; TNF; 1.  
 CC PROSITE; PS00251; TNF\_1; 1.  
 CC PROSITE; PS50049; TNF\_2; 1.  
 CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.  
 KW CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 1 22  
 FT TRANSMEM 23 46  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 47 261  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 178 218  
 FT CARBOHYD 240 240  
 FT N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787FD CRC64;

Query Match 10.5%; Score 176.5; DB 1; Length 261;  
 Best Local Similarity 24.2%; Pred. No. 7.9e-08;  
 Matches 70; Conservative 54; Mismatches 122; Indels 43; Gaps 13;

QY 33 PPPPHAPPPAASRSMFVALLGLL-GQVCSVALFFYFRAQMDPNRISEDTGHCYRIL 91  
 DB 8 PPSRVATGPPVSMKIFMYLLVFLTOMIGSALFAVYLHRLD--KIEDE-----R 57  
 QY 92 RLHENADFDT--TLESODTKLIPDSRCRIKQAFQAVQKELQHVGSQHIRAEKAMVDG 149  
 DB 58 NLHEDFVFKTQRCNKGGSLLNCEIRSFEDLVDMQ----NKEYKKENFE- 112  
 QY 150 SWLDLAKRSKLEAQPFAHITINATIPSGSKVSLSSWYHGRGWAKISN--MTFSNGK-L 206  
 DB 113 -----MHKGDQEPQIAAHVISEAS-----SKTTSVLQW-APKGYITLSNNLVLENGKQL 161  
 QY 207 IVNQDGFYLYANICRHRHETSGDLATAYLQMLVYVTKTSIKIP--SSHTLMKGGSTKYW 264  
 DB 162 AVKROGFYIYQVTPCSNR-----ETLSQAPFTIASLCKSPSGSERILLRAANTH-- 212  
 QY 265 SGNSEPHFYSINVGPFKLRSGEISIEVSNPSLLDPDQDATYFGAKV 313  
 DB 213 SSSKPCQSQSIHLGGVFELOSGASVFNVDPSQVSHGCTGFTSFGLLKL 261

RESULT 8  
 ID FASL\_RAT STANDARD; PRT; 278 AA.  
 AC P36940;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE FAS antigen ligand.  
 GN TNFSF6 OR APTLGI OR FASL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94084792; PubMed=7505205;  
 RA Suda T., Takahashi T., Golstein P., Nagata S.;  
 RT "Molecular cloning and expression of the Fas ligand, a novel member  
 RT of the tumor necrosis factor family.";  
 RL Cell 75:1169-1178(1993).  
 CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
 CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
 CC CYTOTOXIC T CELL-MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
 CC FAS-ANTIGEN-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
 CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
 CC T CELLS, OR BOTH.

CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED  
 CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FROM THE CELL  
 CC SURFACE.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND  
 CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,  
 CC KIDNEY AND LUNG.  
 CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; U03470; A052129.1; -  
 CC HSSP; P01375; 4FSV.  
 CC InterPro; IPR003263; TNF\_5.  
 CC InterPro; IPR003636; TNF\_abc.  
 CC InterPro; IPR000478; TNF\_family.  
 CC Pfam; PF00229; TNF; 1.  
 CC ProDom; PD002012; TNF\_abc; 1.  
 CC ProDom; PD008600; TNF\_5; 1.  
 CC SMART; SM00207; TNF; 1.  
 CC PROSITE; PS00251; TNF\_1; 1.  
 CC PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.  
 FT DOMAIN 1 77  
 FT TRANSMEM 78 99  
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT EXTRACELLULAR (POTENTIAL).  
 FT PRO-RICH.  
 FT POLY-PRO.  
 FT BY SIMILARITY.  
 FT DISULFID 199 230  
 FT CARBOHYD 116 116  
 FT CARBOHYD 247 247  
 FT CARBOHYD 257 257  
 FT N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;

Query Match 10.4%; Score 175.5; DB 1; Length 278;  
 Best Local Similarity 20.3%; Pred. No. 1e-07;  
 Matches 64; Conservative 47; Mismatches 106; Indels 99; Gaps 10;

QY 21 GPCAGEPGLHAPPPHAPPPAASRSM-----FVALLGLL 57  
 DB 39 GPGQRPPP-PPPPSPPLPPSPPLPLPLKKNIELMLPVPFFVVALVGMGL 96  
 QY 58 GQVCSVALFFYFRAQMDPNRISEDTGHCYRILRLHENADFDTTLESQDTKLIPDSR 117  
 DB 97 G-----MYQLFHLQKELAELEFTHSL-RVSSFEKQIANPSTFETKKPRSV----- 143  
 QY 118 RIKQAFQAVQKELQHVGSQHIRAEKAMVDGSLDAKRSKLEAQPFAHITINATIPS 177  
 DB 144 -----AHLTGPR----- 151  
 QY 178 GSHKVSLSWYHGRGWAKISNMTFSNGKLVNODGFYLYANICRHRHETSGDLATAYLQ 237  
 DB 152 -SRISPL-EMEDTYGTALISGVKVKGGVLINAGLYFVYSKRYFRQSCN-----SQPLS 205  
 QY 238 LMVYVTKTSIKIPSSHTLMKGGSTKYWNSGSEPHFYSINVGPFKLRSGEISIEVSNPS 297  
 DB 206 HKVYM--RNFYFGDLVLMEEKLNCT-TGQIWAHSSVGLAVFNLTADVHLVNVISQLS 262  
 QY 298 LDDPDQDATYFGAKV 313  
 DB 263 LINFESKTFEGLYKL 278

RESULT 9  
 TNF5\_HUMAN STANDARD; PRT; 261 AA.  
 ID TNF5\_HUMAN

AC DT  
 DT 01-APR-1993 (Rel. 25; Created)  
 DT 01-APR-1993 (Rel. 25; Last sequence update)  
 DE 16-OCR-2001 (Rel. 40; Last annotation update)  
 DE CD40 ligand (CD40-L) (TNF-related activation protein) (TRAP) (T cell antigen gp39) (CD134 antigen).  
 GN TNFSF5 OR CD40LG OR CD40L OR TRAP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=93076854; PubMed=1280226;  
 RA Graf D., Korthauer U., Mages H.W., Senger G., Krocsek R.A.;  
 RT "Cloning of TRAP, a ligand for CD40 on human T cells.";  
 RL Eur. J. Immunol. 22:3191-3194(1992).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=93049181; PubMed=1385114;  
 RA Hollenbaugh D., Grosmaire L.S., Kullas C.D., Chalupny J.N.,  
 RA Briesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,  
 RA Aruffo A.;  
 RT "The human T cell antigen gp39, a member of the TNF gene family, is a  
 RT ligand for the CD40 receptor: expression of a soluble form of gp39  
 RT with B cell co-stimulatory activity.";  
 RL EMBO J. 11:4313-4321(1992).  
 RN [3]  
 RN SEQUENCE FROM N.A., AND VARIANTS HIGH1 128-ARG-GLY-129 AND PRO-235.  
 RX MEDLINE=93145330; PubMed=7678782;  
 RA Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatovich A.,  
 RA Nonoyama S., Bajorath J., Grosmaire L.S., Stenkamp R., Neubauer M.,  
 RA Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., Ochs H.D.;  
 RT "The CD40 ligand, gp39, is defective in activated T cells from  
 RT patients with X-linked hyper-IgM syndrome.";  
 RL Cell 72:291-300(1993).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=93094757; PubMed=1281209;  
 RA Spriggs M.K., Armitage R.J., Strockbine L., Clifford K.N.,  
 RA Macduff B.W., Sato T.A., Maliszewski C.R., Fanslow W.C.;  
 RT "Recombinant human CD40 ligand stimulates B cell proliferation and  
 RT immunoglobulin E secretion.";  
 RL J. Exp. Med. 176:1543-1550(1992).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=93138085; PubMed=7678552;  
 RA Gauchat J.F.M., Aubry J., Mazzei G.J., Life P., Jomotte T., Elson G.,  
 RA Bonnefoy J.Y.;  
 RT "Human CD40-ligand: molecular cloning, cellular distribution and  
 RT regulation of expression by factors controlling IgE production.";  
 RL FEBS Lett. 315:259-266(1993).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RA Shigematsu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,  
 RA Matsuda I.;  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.  
 RX MEDLINE=96131874; PubMed=8589998;  
 RA Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,  
 RA Chess L., Thomas D.;  
 RT "2-A crystal structure of an extracellular fragment of human CD40  
 RT ligand.";  
 RL Structure 3:1031-1039(1995).  
 RN [8]  
 RN 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.  
 RX MEDLINE=98266353; PubMed=9605317;  
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 RT with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 RN [9]  
 RN VARIANTS HIGH1 ARG-36 AND GLY-140.  
 RX MEDLINE=93156839; PubMed=7679206;  
 RA Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,  
 RA Malcolm S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,  
 RA Krocsek R.A.;  
 RT "Defective expression of T-cell CD40 ligand causes X-linked  
 RT immunodeficiency with hyper-IgM.";  
 RL Nature 361:539-541(1993).  
 RN [10]  
 RN VARIANTS HIGH1 GLU-123.  
 RX MEDLINE=93156840; PubMed=8094231;  
 RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,  
 RA de Saint Basile G.;  
 RT "CD40 ligand mutations in X-linked immunodeficiency with hyper-IgM.";  
 RL Nature 361:541-543(1993).  
 RN [11]  
 RN VARIANTS HIGH1 PRO-155; ASP-211 AND VAL-227.  
 RX MEDLINE=93174270; PubMed=7679801;  
 RA Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,  
 RA Copeland N.G., Bedell M.A., Edelhoff S., Distcheche C.M.,  
 RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;  
 RT "CD40 ligand gene defects responsible for X-linked hyper-IgM  
 RT syndrome.";  
 RL Science 259:990-993(1993).  
 RN [12]  
 RN VARIANTS HIGH1 ALA-126; ARG-140 AND GLU-144.  
 RX MEDLINE=95233438; PubMed=7717401;  
 RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnoli D.,  
 RA Galliani G., Mantuano E., Fasth A., Andersson B., Zegers B.J.M.,  
 RA Cagnani G., Reznick I., Levy J., Zan-Bar I., Porat Y., Alro P.,  
 RA Plebani A., Vezzoni P., Notarangelo L.D.;  
 RT "Characterization of nine novel mutations in the CD40 ligand gene in  
 RT patients with X-linked hyper-IgM syndrome of various ancestry.";  
 RL Am. J. Hum. Genet. 56:898-906(1995).  
 RN [13]  
 RN VARIANTS HIGH1 PRO-155 AND VAL-227, AND VARIANT ARG-219.  
 RX MEDLINE=96133533; PubMed=8550833;  
 RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,  
 RA Gattl R.A., Derauf D.C., Belmont J.W., Conley M.E.;  
 RT "A single strand conformation polymorphism study of CD40 ligand.  
 RT Efficient mutation analysis and carrier detection for X-linked hyper  
 RT IgM syndrome.";  
 RL J. Clin. Invest. 97:196-201(1996).  
 RN [14]  
 RN VARIANTS HIGH1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.  
 RX MEDLINE=97295077; PubMed=9150729;  
 RA Nonoyama S., Shigematsu M., Toru H., Seyama K., Nunoi H., Neubauer M.,  
 RA Yata J.-I., Ochi H.D.;  
 RT "Mutations of the CD40 ligand gene in 13 Japanese patients with  
 RT X-linked hyper-IgM syndrome.";  
 RL Hum. Genet. 99:624-627(1997).  
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-  
 CC STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.  
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+  
 CC T-LYMPHOCYTES.  
 CC -1- DISEASE: DEFECTS IN TNFSF5 ARE THE CAUSE OF AN X-LINKED  
 CC IMMUNODEFICIENCY WITH HYPER-IgM (HIGM1); AN IMMUNOGLOBULIN ISOTYPE  
 CC SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM  
 CC IgM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES  
 CC PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)  
 CC RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING  
 CC PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO  
 CC CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH  
 CC INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,  
 CC WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -1- DATABASE: NAME=CD40Lbase;  
 CC NOTE-European CD40L defect database (mutation db);







Db 112 -----MKGDDPRVAHVISEAS-----SSTASVLQW-APKGYTTSNVLNLTENGKQ 159  
Qy 206 LIVNQDGEYIYANICPRHHTSGDLATEYLQMLVYVTKTSIKIP--SSHTLMGGSTKY 263  
Db 160 LAVKROGLYIYAVQVTCNSREASQAP-----FTASLCLHSPSGSERVLLRAANAR- 211  
Qy 264 WSGNSEHFYINVGGFKLRSGEISIEVSNPLSDPDQDATYFGAFKV 313  
Db 212 -SSSKPCQOQHILGGVFEHPGASVFVNDPDSOVSHGTGFTSGLLKL 260

RESULT 11  
TNFA\_CAVPO  
ID TNFA\_CAVPO STANDARD; PRT; 234 AA.  
AC P51435;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
GN TNF OR TNFA.  
OS Cavia porcellus (Guinea pig).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
NCBI\_TaxID=10141;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN-HARTLEY; TISSUE-Lung;  
RA Yuan H.T., Kelly F.J., Bingle C.D.;  
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN-DUNKIN-HARTLEY;  
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;  
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis  
factor-alpha";  
RL Am. J. Physiol. 273:L574-L530(1997).  
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE  
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CC CONDITIONS.  
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).  
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; U39839; AAB06492.1; -  
EMBL; U77036; AAB19210.1; -  
HSSP; P06804; 2TNF.  
InterPro; IPR003636; TNF\_abc.  
InterPro; IPR000478; TNF\_family.  
Pfam; PF00229; TNF; 1.  
PRINTS; PR01234; TNCRSISFCT.  
ProDom; PD002012; TNF\_abc; 1.  
SMART; SM00207; TNF; 1.  
PROSITE; PS00251; TNF\_1; 1.  
PROSITE; PS0049; TNF\_2; 1.  
PROSITE; PS0049; TNF\_2; 1.

KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
FT PROPEP 1 79 BY SIMILARITY.  
FT CHAIN 80 234 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DISULFID 147 178 BY SIMILARITY.  
SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 8.7%; Score 146; DB 1; Length 234; A  
Best Local Similarity 25.4%; Pred. No. 2.7e-05;  
Matches 50; Conservative 30; Mismatches 75; Indels 42; Gaps 8;

Qy 134 IVGSQHIAEAKAMVDCSWLDLAKRSKLEA-----QPPAHLTINATIPSGSHKVSLS 186  
Db 55 VIGPQ--REEQFSGPPFRPLAQTUTLSASQNDNDKPKVAHVAN-----QQAEEELQ 105  
Qy 187 WYHGRGNAKISN-WTFSGKGLIVNODGFFYLYANICPRHHTSGDLATEYLQMLVYVTKT 245  
Db 106 WLSKRANALLANGMLSDNQLVVPDGLYLYISQVLFK-----GGCCPSYLLLTHTVSRL 160  
Qy 246 SIKIPSSHTLN-----KGSSTKYNSEEFHYSINVGFFKLRSGEISIEV 293  
Db 161 AVSYPEKVNLLSAIKSPCKQETPEGAERKPW-----YEPIYLGGVFOLQKGRLSAEV 213  
Qy 294 SNPSLLD-PQDDATYFG 309  
Db 214 NLPQYLDFAFADSGQIYFG 230

RESULT 12  
TNF5\_CANFA  
ID TNF5\_CANFA STANDARD; PRT; 260 AA.  
AC O97626;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE CD40 ligand.  
GN TNF5 OR CD40LG OR CD40L.  
OS Canis familiaris (Dog).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
NCBI\_TaxID=9615;  
[1]  
RN SEQUENCE FROM N.A.  
RA Hosie M.H., Willett B.J.;  
RT "Adjuvant properties of canine CD40L";  
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-  
CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.  
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).  
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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modified and this statement is not removed. Usage by and for commercial  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; AF086711; AAD04375.1; -  
HSSP; P29965; ITALY.  
InterPro; IPR003263; TNF\_5.  
InterPro; IPR000478; TNF\_family.  
Pfam; PF00229; TNF; 1.  
ProDom; PD008600; TNF\_5; 1.  
SMART; SM00207; TNF; 1.  
PROSITE; PS00251; TNF\_1; 1.  
PROSITE; PS0049; TNF\_2; 1.  
CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor.  
CYTOPLASMIC (POTENTIAL).  
DOMAIN 1 22

FT TRANSMEM 23 46 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT DOMAIN 47 260 (POTENTIAL).  
FT DISULFID 177 217 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 239 239 POTENTIAL.  
SQ SEQUENCE 260 AA; 28688 MW; 604F69A19E98EB70 CRC64;  
  
Query Match 8.6%; Score 145; DB 1; Length 260;  
Best Local Similarity 23.1%; Pred. No. 3.7e-05;  
Matches 65; Conservative 58; Mismatches 112; Indels 46; Gaps 14;  
  
QY 42 PAASRMFVALGLGL-GGVGSVALFFYFRAQMPDNRISEDTGHCIIYRILRLHENADPQ 100  
D 17 PPSMKIFWYLTFLITOMIGSALFAVYLHRRLD-KIEDE-----RNLYEDFVEM 66  
  
QY 101 DTTLSQ--DTKLIPDSRRIRKQAFQVOKELQHVIGSOHRAEKAMVDGSLDLAKRS 158  
D 67 KTLQCKNKGESLNLCEIKSQFEAF-----LKEITLNMNMKKEENIA-----MORG 115  
  
159 KLEAOPFAHLTNATDIPSGSHKVSLSWYHDSGNAKISN--MTFSNGK-LIVNODGFY 215  
D 116 DQDPTAAHVISEASNP-----SVLRW-APGYTISNLVSLNGQLAVKRGGLY 169  
  
QY 216 LYANICFRHETSGDLATEYLQLMVYVTKTSIKIPS--SHTLMKGGSTYKWSNPF-PHF 272  
D 170 VYAVQVTFCSNRAASSQAP-----FVASLCLHSPSGSTERVLLRAASSR---GSSKPCGQ 219  
  
QY 273 YSINVGGFKLSGGEISIEVSNPSLLDPDQATYFQAKV 313  
D 220 QSHLGGVFLHPGASVFFVNVTPDSQVSHGTGFTSFGLKL 260

## RESULT 13

TNFA\_MOUSE  
ID TNFA\_MOUSE STANDARD; PRT; 235 AA.  
AC P06804; Q62326;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-MAR-1989 (Rel. 10, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Tumor necrosis factor precursor (TNF-alpha) (Cachectin).  
GN TNF OR TNFA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
SEQUENCE FROM N.A.  
MEDLINE=88224564; PubMed=2836146;  
RA Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;  
RT "Cloning and expression in Escherichia coli of the gene for mouse  
RT tumor necrosis factor.";  
RL DNA 7:193-201(1988).  
RN [2]  
SEQUENCE FROM N.A.  
MEDLINE=85298296; PubMed=3898078;  
RX Pennica D., Hayflick J.S., Brinman T.S., Palladino M.A.,  
RA Goeddel D.V.;  
RT "Cloning and expression in Escherichia coli of the cDNA for murine  
RT tumor necrosis factor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).  
RN [3]  
SEQUENCE FROM N.A.  
RX MEDLINE=86149365; PubMed=2419912;  
RA Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,  
RA Cerami A.;  
RT "Identification of a common nucleotide sequence in the  
RT 3'-untranslated region of mRNA molecules specifying inflammatory  
RT mediators.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).  
RN [4]  
SEQUENCE FROM N.A.  
RX MEDLINE=85242112; PubMed=2989794;  
RX Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,

RA Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,  
RA Ruyschaert M.-R., Fiers W.;  
RT "Molecular cloning of mouse tumour necrosis factor cDNA and its  
RT eukaryotic expression.";  
RL Nucleic Acids Res. 13:4417-4429(1985).  
RN [5]  
SEQUENCE FROM N.A.  
RX MEDLINE=87298639; PubMed=3040015;  
RA Shakhov A.N., Nedospasov S.A.;  
RT "Molecular cloning of genes coding for tumor necrosis factor.  
RT Complete nucleotide sequence of the genome copy of TNF-alpha in  
RL mice.";  
RL Bioorg. Khim. 13:701-705(1987).  
RN [6]  
SEQUENCE FROM N.A.  
RX MEDLINE=88067722; PubMed=3684584;  
RA Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;  
RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha  
RT (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";  
RL Nucleic Acids Res. 15:9083-9084(1987).  
RN [7]  
SEQUENCE FROM N.A.  
RC STRAIN-CTS, AND MOD;  
RX MEDLINE=96013654; PubMed=7560085;  
RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,  
RA Takekawa K., Ogihara T.;  
RT "Identification of a new susceptibility locus for insulin-dependent  
RT diabetes mellitus by ancestral haplotype congenic mapping.";  
RL J. Clin. Invest. 96:1936-1942(1995).  
RN [8]  
SEQUENCE OF 80-99.  
RX MEDLINE=91097531; PubMed=2268312;  
RA Sherry B., Juc D.-M., Zentella A., Cerami A.;  
RT "Characterization of high molecular weight glycosylated forms of  
RT murine tumor necrosis factor.";  
RL Biochem. Biophys. Res. Commun. 173:1072-1078(1990).  
RN [9]  
SEQUENCE OF 70-87.  
RX MEDLINE=89380231; PubMed=2777790;  
RA Cseh K., Beutler B.;  
RT "Alternative cleavage of the cachectin/tumor necrosis factor  
RT propeptide results in a larger, inactive form of secreted protein.";  
RL J. Biol. Chem. 264:16256-16260(1989).  
RN [10]  
IDENTIFICATION OF MEMBRANE-BOUND FORM.  
RX MEDLINE=88165056; PubMed=3349526;  
RA Kriegler M., Perez X., Defay K., Albert I., Lu S.D.;  
RT "A novel form of TNF/cachectin is a cell surface cytotoxic  
RT transmembrane protein: ramifications for the complex physiology of  
RL TNF.";  
RL Cell 53:45-53(1988).  
RN [11]  
X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.  
RX MEDLINE=99190964; PubMed=10089307;  
RA Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;  
RT "The structure of mouse tumour necrosis factor at 1.4 A resolution:  
RT towards modulation of its selectivity and trimerization.";  
RL Acta Crystallogr. D 55:772-778(1999).  
CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CC CONDITIONS.  
CC -1- SUBUNIT: HOMOTRIMER.  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM.  
CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
CC PROTEOLYTIC PROCESSING.  
CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.



CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.

-I- SUBUNIT: HOMOTRIMER.

-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.

-I- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.

-I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.

-I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; X55966; CAA39437.1; - -  
DR EMBL; X55152; CAA38952.1; - -  
DR EMBL; X56756; CAA40076.1; - -  
DR EMBL; A19163; CAA01445.1; - -  
DR PIR; S13114; S13114.  
DR PIR; S20661; S20661.  
DR PIR; JH0529; JH0529.  
DR HSSP; P01375; 4T5V.  
DR InterPro; IPR003636; TNF-abc.  
DR InterPro; IPR000478; TNF-family.

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DR PRODOM: PD002012; TNF_abc; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
KW Cytokine; Cytotoxic; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 77
FT CHAIN 78 234
FT TRANSHEM 36 56
FT DLSULFID 146 178
FT CARBOHYD 96 96
FT CONFLICT 63 63
SQ SEQUENCE 234 AA; 25536 MW; 4BCF8CCAB7956B88 CRC64;
      TUMOR NECROSIS FACTOR.
      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
      BY SIMILARITY.
      N-LINKED (GLCNAC. . . ) (POTENTIAL).
      MISSING (IN REF. 1).
Query Match      8.18; Score 137; DB 1; Length 234;
Best Local Similarity 26.18; Pred. No. 0.00016;
Matches 52; Conservative 30; Mismatches 71; Indels 46; Gaps 10;

QY 134 IVGSGHIAERAAKVDGWS--LDLAKRSKLEA---QPPAHLTINATIPSGSHKVSLSW 187
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 VIGPQ--REEQSPAGSPNRPVQTLTRSSSQASNKPVAHVAN-----ISAP 100
      : : : : : : : : : : : : : : : : : : : : : : : :

QY 188 YHGRGNAKISNMTFSNG-----KLIVNQDGFYLYANICFRHH-----ETSGDL 231
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 GQLRWGDSYANALMANGVELKNDQLVPTDGLIYISQVLFGRGCPSTPLFLHTTISR 160
      : : : : : : : : : : : : : : : : : : : : : : : :

QY 232 ATEYLQLMVMYVTKSIKIPSSHTLMKGSTKYWGSNSEFHYISNVGGFFFLRSGEETSI 291
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 AVSY-QTKVNIL-SAIKSPCHREILEGAERAPW-----YEPIYOGGVFQLEKGRDL 211
      : : : : : : : : : : : : : : : : : : : : : : : :

QY 292 EVSNPSLLD-PDQDATYFG 309
      : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 EINLPEYLDYAESGVQYFG 230
      : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: October 10, 2002, 16:04:50
Job time : 41.2379 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 102.166 Seconds  
(without alignments)  
536.769 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEMG.....LLDPDQDATYGAFAKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Archived: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Match | Length | ID | Description |
|------------|--------|-------|--------|----|-------------|
| 1          | 1422   | 84.4  | 270    | 4  | Q96Q17      |
| 2          | 1409   | 83.6  | 313    | 11 | Q9RIY0      |
| 3          | 1396.5 | 82.9  | 318    | 11 | Q9ESE2      |
| 4          | 1271   | 75.4  | 287    | 11 | Q9JJK9      |
| 5          | 909    | 53.9  | 199    | 11 | Q9JJK8      |
| 6          | 262    | 15.5  | 53     | 11 | Q9I219      |
| 7          | 240.5  | 14.3  | 214    | 13 | Q9DDZ5      |
| 8          | 216.5  | 12.8  | 287    | 13 | Q9QWT9      |
| 9          | 200    | 11.9  | 282    | 6  | Q9BEA8      |
| 10         | 200    | 11.9  | 282    | 6  | Q9SM04      |
| 11         | 199    | 11.8  | 282    | 6  | Q95N10      |
| 12         | 186    | 11.0  | 280    | 6  | Q9MYL6      |
| 13         | 184.5  | 10.9  | 280    | 6  | Q9BDM5      |
| 14         | 182.5  | 10.8  | 280    | 6  | Q9BDN1      |
| 15         | 169.5  | 10.1  | 261    | 6  | Q9BDN3      |
| 16         | 167.5  | 9.9   | 261    | 6  | Q9BDM3      |

|    |       |     |     |    |        |
|----|-------|-----|-----|----|--------|
| 17 | 155.5 | 9.2 | 261 | 6  | Q9BDC7 |
| 18 | 155   | 9.2 | 272 | 13 | Q9I8D8 |
| 19 | 145.5 | 8.6 | 239 | 11 | Q9QYH9 |
| 20 | 145   | 8.6 | 174 | 4  | Q95150 |
| 21 | 144   | 8.5 | 232 | 11 | Q35853 |
| 22 | 143   | 8.5 | 240 | 6  | Q9BDM7 |
| 23 | 139.5 | 8.3 | 215 | 11 | Q99ND1 |
| 24 | 137.5 | 8.2 | 156 | 11 | Q912L4 |
| 25 | 136   | 8.1 | 234 | 6  | Q28320 |
| 26 | 134.5 | 8.0 | 310 | 11 | Q9JMI0 |
| 27 | 134   | 8.0 | 157 | 4  | Q43647 |
| 28 | 134   | 8.0 | 204 | 4  | Q96LD2 |
| 29 | 133   | 7.9 | 149 | 6  | Q97543 |
| 30 | 133   | 7.9 | 191 | 6  | Q9MYZ2 |
| 31 | 133   | 7.9 | 232 | 4  | Q9UIV3 |
| 32 | 131.5 | 7.8 | 216 | 11 | Q70332 |
| 33 | 130   | 7.7 | 217 | 11 | Q9ERG6 |
| 34 | 128   | 7.6 | 234 | 6  | Q9RTJ3 |
| 35 | 127.5 | 7.6 | 217 | 6  | Q9BEC5 |
| 36 | 127.5 | 7.6 | 235 | 11 | Q9J127 |
| 37 | 127.5 | 7.6 | 235 | 11 | Q9J126 |
| 38 | 127.5 | 7.6 | 310 | 11 | Q9JMI1 |
| 39 | 126   | 7.5 | 149 | 6  | Q97538 |
| 40 | 126   | 7.5 | 149 | 6  | Q9RTG8 |
| 41 | 125   | 7.4 | 216 | 6  | Q9BEC9 |
| 42 | 124   | 7.4 | 250 | 6  | Q9XT47 |
| 43 | 120.5 | 7.2 | 217 | 6  | Q9BEG1 |
| 44 | 120.5 | 7.2 | 217 | 6  | Q9BEG0 |
| 45 | 120   | 7.1 | 260 | 11 | Q9Z2V2 |

ALIGNMENTS

RESULT 1

Q96Q17 PRELIMINARY; PRT; 270 AA.  
AC Q96Q17;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE FRANKL 2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ikeda T., Kuroyama H., Hirokawa K.;  
RT "Human RANKL isoform.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB061227; BAB71768.1; -  
SQ SEQUENCE 270 AA; 30522 MW; 5C7754CE32E6F368 CRC64;

Query Match 84.4%; Score 1422; DB 4; Length 270;  
Best Local Similarity 100.0%; Pred. No. 1.1e-121;  
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|----|-----|--|-----|
| QY | 48  | MFVALLGIGLGVVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDTTLESQ | 107 |
| Db | 1   | MFVALLGIGLGVVCSVALFFYFRAQMDPNRISEDTGTCIYRILRLHENADFDTTLESQ | 60  |
| QY | 108 | DTKLIPDSRRIKQAFQGVQKLOHIVGSHIRAEKAMVDGSLDLAKRSKLEAQPFAH    | 167 |
| Db | 61  | DTKLIPDSRRIKQAFQGVQKLOHIVGSHIRAEKAMVDGSLDLAKRSKLEAQPFAH    | 120 |
| QY | 168 | LTINATDIPSGSHKVSLSWYHDSRWAKISNMTFSNGKLIVNQDGFYLLYANICFRHET | 227 |
| Db | 121 | LTINATDIPSGSHKVSLSWYHDSRWAKISNMTFSNGKLIVNQDGFYLLYANICFRHET | 180 |
| QY | 228 | SGDLATYQLMVTYTKTSIKIPSSHTLMKGGSTKYSGNSERHFYSINVGGFKLRSGE   | 287 |
| Db | 181 | SGDLATYQLMVTYTKTSIKIPSSHTLMKGGSTKYSGNSERHFYSINVGGFKLRSGE   | 240 |

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Qy 288 EISIEVSNPSLLDPDQDATYFGAFKVRDID 317
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Db 241 EISIEVSNPSLLDPDQDATYFGAFKVRDID 270

RESULT 2
Q9RIY0 PRELIMINARY; PRT; 313 AA.
AC Q9RIY0
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OSTEOCLAST DIFFERENTIATION FACTOR.
GN TNFSF11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=129;
MEDLINE=99214075; PubMed=10196481;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RT "Cloning and characterization of the gene encoding mouse osteoclast
RT differentiation factor.";
RL Gene 230:121-127(1999).
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR HSSP; P50591; 1D0G.
DR MGD; MGI:1100089; Tnfsf11.
DR InterPro; IPR003263; TNF_5.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 313 AA; 37419 MW; 37D530B8BFC2842E CRC64;

Query Match 83.6%; Score 1409; DB 11; Length 313;
Best Local Similarity 84.3%; Pred. No. 2.1e-120;
Matches 268; Conservative 16; Mismatches 28; Indels 6; Gaps 3;

Qy 1 MRRASRDYTKYLRGSEMGPGAPHEGLH-APPPHAPPAPPAASRSMFVALLGLGQ 59
      |||||||
Db 1 MRRASRDYTKYLRGSEMGPGAPHEGLH-APPPHAPPAPPAASRSMFVALLGLGQ 60

60 VVCSVALFFYFRAQMDPNRISEDTGTHCYRIILRLHENADFQDTTLESODTKLIPDCRR 119
      |||||||
Db 61 VVCSVALFFYFRAQMDPNRISEDTGTHCYRIILRLHENADFQDTTLESODTKLIPDCRR 120

120 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATIPSGS 179
      |||||||
Db 121 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATIPSGS 180

180 HKVLSLSSYHWRGWAQKISNMTFSNGKLVNODGFYLYANICFRHETSGDLATYQLM 239
      |||||||
Db 181 HKVLSLSSYHWRGWAQKISNMTFSNGKLVNODGFYLYANICFRHETSGDLATYQLM 240

240 VYVTKTSIKIPSSHTLMKGGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299
      |||||||
Db 241 VYVTKTSIKIPSSHTLMKGGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 300

300 DPQDQATYFGAFKVRDID 317
      |||||||
Db 301 DPQDQATYFGAFKVRDID 318

RESULT 4
Q9JJK9 PRELIMINARY; PRT; 287 AA.
AC Q9JJK9
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 2.
GN TNFSF11 OR RANKL 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=21150053; PubMed=11250921;

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ID Q9ESE2 PRELIMINARY; PRT; 318 AA.
AC Q9ESE2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=20540945; PubMed=11092398;
RA Xu J.K., Tan J., Huang L., Gao X.H., Laird R., Liu D., Wysocki S.,
RA Zheng M.H.;
RT "Cloning, sequence and functional characterization of the rat
RT homologue of receptor activator of NF-kB ligand.";
RL J. Bone Miner. Res. 15:2178-2186(2000).
DR EMBL; AF187319; WAGI7031.1; -.
DR HSSP; P50591; 1D0G.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR000478; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD008600; TNF_5; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD098F CRC64;

Query Match 82.9%; Score 1396.5; DB 11; Length 318;
Best Local Similarity 82.4%; Pred. No. 3e-119;
Matches 262; Conservative 19; Mismatches 36; Indels 1; Gaps 1;

Qy 1 MRRASRDYTKYLRGSEMGPGAPHEGLH-APPPHAPPAPPAASRSMFVALLGLGQ 59
      |||||||
Db 1 MRRASRDYTKYLRGSEMGPGAPHEGLH-APPPHAPPAPPAASRSMFVALLGLGQ 60

60 VVCSVALFFYFRAQMDPNRISEDTGTHCYRIILRLHENADFQDTTLESODTKLIPDCRR 119
      |||||||
Db 61 VVCSVALFFYFRAQMDPNRISEDTGTHCYRIILRLHENADFQDTTLESODTKLIPDCRR 120

120 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATIPSGS 179
      |||||||
Db 121 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATIPSGS 180

180 HKVLSLSSYHWRGWAQKISNMTFSNGKLVNODGFYLYANICFRHETSGDLATYQLM 239
      |||||||
Db 181 HKVLSLSSYHWRGWAQKISNMTFSNGKLVNODGFYLYANICFRHETSGDLATYQLM 240

240 VYVTKTSIKIPSSHTLMKGGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 299
      |||||||
Db 241 VYVTKTSIKIPSSHTLMKGGSTKYNSGSEFHFYSINVGFFKLRSGEISIEVSNPSLL 300

300 DPQDQATYFGAFKVRDID 317
      |||||||
Db 301 DPQDQATYFGAFKVRDID 318

RESULT 4
Q9JJK9 PRELIMINARY; PRT; 287 AA.
AC Q9JJK9
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KB LIGAND 2.
GN TNFSF11 OR RANKL 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=21150053; PubMed=11250921;

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DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00229; TNF; 1.
DR ProDom: PD002012; TNF_abc; 1.
DR ProDom: PD008600; TNF_5; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR SEQUENCE 199 AA; 22150 MW; 401C13EB5B8CE166 CRC64;
SQ
Query Match 53.9%; Score 909; DB 11; Length 199;
Best Local Similarity 85.4%; Pred. No. 4.8e-75;
Matches 170; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 119 IKAQFAGVQKELQHVGSQHIAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSG 178
:|||||N:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 1 MKQAFQAGVQKELQHVGPORFSGAPMMGSLDVAQRGKPEAQPFAHLTINAAIPSG 60

QY 179 SHKVSLSWYHGRGWAQKISNMTSNGKLIIVNQDGFYYLYANICFRHHETSGDLATEYLQ 238
|||||N:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 61 SHKVTLSWYHGRGWAQKISNMTLSNGKLIIVNQDGFYYLYANICFRHHETSSVPTDYLQ 120

QY 239 MVYVTKTSIKIPSSHTLMKGGSTKYKWSGSEFHYISINVGGFKLRGEEISIEVSNPSL 298
|||||N:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 121 MVYVTKTSIKIPSSHNLKMGSTKWSGSEFHYISINVGGFKLRAGEEISIQVSNPSL 180

QY 299 LDPDQDATYFGAFKVRDID 317
|||||N:|:|:|||||:|:|:|||||:|:|:|||||
Db 181 LDPDQDATYFGAFKVRQDID 199

RESULT 6
Q91Z19 PRELIMINARY; PRT; 53 AA.
ID Q91Z19
AC Q91Z19;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TNFSF11 (FRAGMENT).
DE TNFSF11.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=F344;
RA Ogden P.R.; Kim N.; van Wesenbeeck L.; Mackay C.A.; Mason-Savas A.;
RA Safadi F.F.; Popoff S.N.; Lengner C.; van Hul W.; Choi Y.; Marks S.C.;
RT "Evidence that the rat osteopetrotic mutation toothless (tl) is not in
RT the tnfsf11 (TRANCE, RANKL, ODF, OPGL) gene."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF425669; AAL23963.1;
FT NON_TPR 1
FT SEQUENCE 53 AA; 5876 MW; 8A71E32F2B6A9410 CRC64;
SQ
Query Match 15.5%; Score 262; DB 11; Length 53;
Best Local Similarity 90.6%; Pred. No. 8.3e-17;
Matches 48; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 265 SGNSEFHYISINVGGFKLRGEEISIEVSNPSLLDPDQDATYFGAFKVRDID 317
|||||N:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||
Db 1 SGNSEFHYISINVGGFKLRAGEEISIVSNPSLLDPDQDATYFGAFKVRQMD 53

RESULT 7
Q9DDZ5 PRELIMINARY; PRT; 214 AA.
ID Q9DDZ5
AC Q9DDZ5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TRAIL-LIKE PROTEIN.
GN TNFSF10L.
OS Brachydanio rerio (zebrafish) (zebra danio).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN  
RP SEQUENCE FROM N.A.  
RA Bobe J., Goetz F.W.;  
RT "Molecular cloning and expression of a TNF receptor and two TNF  
ligands in the fish ovary."  
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).  
DR EMBL: AF250041; RAG47640.1; -;  
DR HSSP: P50591; ID06.  
DR 2FIN; ZDB-GENE-010801-1; tnfsf101.  
DR InterPro: IPR003263; TNF\_5.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF\_1.  
DR ProDom: PD002012; TNF\_abc; 1.  
DR ProDom: PD008600; TNF\_5; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS50049; TNF.2; 1.  
DR SEQUENCE 214 AA; 24093 MW; 98C002474FF691AA CRC64;  
Query Match 14.3%; Score 240.5; DB 13; Length 214;  
Best Local Similarity 28.6%; Pred. No. 5.4e-14;  
Matches 61; Conservative 50; Mismatches 83; Indels 19; Gaps 5;  
QY 118 RIKAFQAGVOKELQHVQSHIPEAKWVDGSLDLAK-RSKLEAPFAHLTINATDIP 176  
Db 2 KLAGIRAKYISKVDSIISKQTLHAARTQTHSYNTGSKFMTVMQPSAHLTLSSASDN 61  
QY 177 S-----GSHKVSLSWYHGRGWAKISNMTFSGKLIYNQDGFYLYANICF 222  
Db 62 SRPOSDMHQPOFDLHQSRHPVHTWANKSGAHLNLTNGRLVRVQDGRYLYSQYVF 121  
QY 223 RHHTS-GLDTEYELQMLVYV-TKTSIKIPSSHTLMKGGSTKYWSGSEHFYSINVGGF 280  
Db 122 RYPSDSDQSSVSHOLVQCIYKTYLNPQ--LLKGVGTKWAPDAEYALHVSVOGGL 179  
QY 281 FKLRSGEISIEVNSPLDPPQDATFGAFKV 313  
Db 180 FELRAGDEVFVSVPSTVMYGEDSSVFGAPRL 212  
RESULT 8  
Q90WT9 PRELIMINARY; PRT; 287 AA.  
AC Q90WT9;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
TNF-RELATED APOPTOSIS INDUCING LIGAND.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN  
RP SEQUENCE FROM N.A.  
RA Bridgman J.T., Johnson A.L.;  
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen  
ovary."  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY057941; AAL23702.1; -;  
DR SEQUENCE 287 AA; 32092 MW; DB06E1C95087B108 CRC64;  
Query Match 12.8%; Score 216.5; DB 13; Length 287;  
Best Local Similarity 24.7%; Pred. No. 1.3e-11;  
Matches 61; Conservative 57; Mismatches 104; Indels 25; Gaps 6;  
QY 80 SEDGTHCIYRIURLHENADFOTTLTLESQDTKLIPDSCRRIRKQAFQAGVOKELQHVQSH 139  
Db 51 SSELRLCLINQOQEGSLEEL-----ISNQSLKLANWIKAYVATVTENVISRSV 102

QY 140 I-RAKAWVDGSLDLAKSKLEAPFAHLTINATDIP-----SGSHKVSLSW 187  
Db 103 VNEAKSYFNISEGQVA--TKLGKPSAHLIFRPQPAQDSSRRFGNLSOSCEHAITRW 160  
QY 188 YHDRGWAKISNMTFSGKLIYNQDGFYLYANICFRHHTSGDLATEYELQMLVYV-TKTS 246  
Db 161 EDSTHSHLQNIYTRDGLRLVRVQAGYVYSQIYFRYSRDAGARVSPQOLVQCIINWTS 220  
QY 247 IKIPSSHTLMKGGSTKYWSGSEHFYSINVGGFFLKRSCEEISIEVNSPLDPPQDAT 306  
Db 221 YSQPI--LLKGVGTRCWAPDAEYALHVSVOGGLFELKAGDELFSVSSLAIDYSDAAS 278  
QY 307 YFGAFKV 313  
Db 279 YFGAPRL 285  
RESULT 9  
Q9BEA8 PRELIMINARY; PRT; 282 AA.  
AC Q9BEA8;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
FAS-LIGAND (FAS LIGAND).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE-2132533; PubMed-11429161;  
RA Muneta Y., Shimoji Y., Inumaru S., Mori Y.;  
RT "Molecular cloning, characterization, and expression of porcine Fas  
ligand (CD95 ligand)."  
RL J. Interferon Cytokine Res. 21:305-312(2001).  
RN  
RP SEQUENCE FROM N.A.  
RA Tsuyuki S., Kono M., Bloom E.T.;  
RT "Cloning and potential utility of porcine Fas ligand: overexpression  
in porcine cells protects them from attack by human cytolytic cells."  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB027297; BAB40919.1; -;  
DR EMBL: AF397407; AAR84408.1; -;  
DR HSSP: P01375; 4TSV.  
DR InterPro: IPR003263; TNF\_5.  
DR InterPro: IPR003636; TNF\_abc.  
DR InterPro: IPR000478; TNF\_family.  
DR Pfam: PF00229; TNF; 1.  
DR PRINTS: PR01234; TNECROSISFCT.  
DR ProDom: PD002012; TNF\_abc; 1.  
DR ProDom: PD008600; TNF\_5; 1.  
DR SMART: SM00207; TNF; 1.  
DR PROSITE: PS00251; TNF.1; 1.  
DR PROSITE: PS50049; TNF.2; 1.  
DR SEQUENCE 282 AA; 31756 MW; 6743DRA1145671PB CRC64;  
Query Match 11.9%; Score 200; DB 6; Length 282;  
Best Local Similarity 23.0%; Pred. No. 3.9e-10;  
Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;  
QY 22 PGAPHEGLHAPPPPPHAPHPAA-----SRSM-----FVA 51  
Db 37 PGRP--GQRRPPPPPPPPPPPTLLPSRPLPLPPPSLKKKDHNGNGLLVNFWFWLVA 94  
QY 52 LLGLGLGVQVCSVALFFVFRQMDPNRISDGTCHYIRILRLHENADFOTTLTLESQDTKL 111  
Db 95 LVGLGLG-----WFQFLHLOKE-----LTLESASQRT----- 124  
QY 112 IPDSCRRIRKQAFQAGVOKELQHVQSHIPEAKWVDGSLDLAKSKLEAPFAHLT-- 169  
Db 125 -----ESSLEKQIGHNLPSEKK-----ELRKVAHLTK 153



QY 170 INATDIPSGSHKVSLSWYHNRGAKISNMTFSGKLIVNODGFYLYANICFRHETSG 229  
 Db 154 PMSRIP-----LEWEDTYGIALVSGVKYMGSLVINDTGLFYVSKYFRGQYCN- 204  
 QY 230 DLATEYLQMLVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEHFYSINVGGFKL 283  
 Db 205 ---NOPLSHKVV-TRNS-RYPQDLVLMGKMMNYCTTGQMWARS-----YLGAVFNLT 252  
 QY 284 RSGEISIEVSNPSLLDPDQDATYFGAFKV 313  
 Db 253 TSADHLYNVSELSLVNFEESTKFFGLYKL 282

RESULT 10  
 Q95M04 PRELIMINARY; PRT; 282 AA.  
 Q95M04;  
 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DE FAS-LIGAND.  
 GN FASL.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID-9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-BRED LANDRACE X LARGE YORKSHIRE WHITE (LW); TISSUE=LIVER;  
 RC Motegi-Ishiyama Y., Nakajima Y., Hoka S., Takagaki Y.;  
 RT "Genomic Sequence Analysis of pig Fas-Ligand Gene."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB069784; BAB64291.1; -  
 SQ SEQUENCE 282 AA; 31722 MW; E54774EBF455127B CRC64;

Query Match 11.9%; Score 200; DB 6; Length 282;  
 Best Local Similarity 23.0%; Pred. No. 3.9e-10;  
 Matches 76; Conservative 42; Mismatches 90; Indels 122; Gaps 14;

QY 22 PGAPHEGLHAPPPHAPHPAA-----SRSM-----FVA 51  
 Db 37 PGRP--GQRRPPPPPPPPPPPTLLPSRPLPPPLPPSLKKRDNHAGLCLLVFMFVLVA 94  
 QY 52 LGLGLGVCSVALFFYFRAQMDPNRISEDTGTCIYRILRHENADFQDTLESQDTKL 111  
 95 LVGLGLG-----MFQLFHLQKE-----LTRELRESASQRT----- 124  
 QY 112 IPDCRRRIKQAFQGAQVQKELQIHVGSOHIRAEKAMVDGSLDLAKRSKLEAQPFAHLT-- 169  
 Db 125 -----ESSLEKQIGHNLPSEKK-----ELRKVAHLTGK 153  
 QY 170 INATDIPSGSHKVSLSWYHNRGAKISNMTFSGKLIVNODGFYLYANICFRHETSG 229  
 Db 154 PMSRIP-----LEWEDTYGIALVSGVKYMGSLVINDTGLFYVSKYFRGQYCN- 204  
 QY 230 DLATEYLQMLVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEHFYSINVGGFKL 283  
 Db 205 ---NOPLSHKVV-TRNS-RYPQDLVLMGKMMNYCTTGQMWARS-----YLGAVFNLT 252  
 QY 284 RSGEISIEVSNPSLLDPDQDATYFGAFKV 313  
 Db 253 TSADHLYNVSELSLVNFEESTKFFGLYKL 282

RESULT 11  
 Q95N10 PRELIMINARY; PRT; 282 AA.  
 Q95N10;  
 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DE FAS LIGAND.

GN FASL.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID-9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhu N., Young Y.;  
 RT "Molecular cloning and characterization of porcine Fas ligand cDNA."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY033634; AAK56449.1; -  
 SQ SEQUENCE 282 AA; 31752 MW; F391212406AE1E7D CRC64;

Query Match 11.8%; Score 199; DB 6; Length 282;  
 Best Local Similarity 22.9%; Pred. No. 4.9e-10;  
 Matches 75; Conservative 43; Mismatches 92; Indels 118; Gaps 13;

QY 22 PGAPHEGLHAPPPHAPHPAA-----FVALL 53  
 Db 37 PGRPQRRPPPPPPPPPPPPPLPSRPLPPPLPPSLKKRDNHAGLCLLVFMFVLVA 96  
 QY 54 GLGLGVCSVALFFYFRAQMDPNRISEDTGTCIYRILRHENADFQDTLESQDTKLIP 113  
 Db 97 GLGLG-----MFQLFHLQKE-----LTRELRESASQRT----- 124  
 QY 114 DSCRRIKQAFQGAQVQKELQIHVGSOHIRAEKAMVDGSLDLAKRSKLEAQPFAHLT--IN 171  
 Db 125 -----ESSLEKQIGHNLPSEKK-----ELRKVAHLTGKPN 155  
 QY 172 ATDIPSGSHKVSLSWYHNRGAKISNMTFSGKLIVNODGFYLYANICFRHETSGDL 231  
 Db 156 SRSIP-----LEWEDTYGIALVSGVKYMGSLVINDTGLFYVSKYFRGQYCN--- 204  
 QY 232 ATEYLQMLVYVTKTSIKIPSSHTLMKGGSTKY-----WSGNSEHFYSINVGGFKLRS 285  
 Db 205 -NOPLSHKVV-TRNS-RYPQDLVLMGKMMNYCTTGQMWARS-----YLGAVFNLTJS 254  
 QY 286 GEEISIEVSNPSLLDPDQDATYFGAFKV 313  
 Db 255 ADHLYNVSELSLVNFEESTKFFGLYKL 282

RESULT 12  
 Q9MYL6 PRELIMINARY; PRT; 280 AA.  
 ID Q9MYL6  
 AC Q9MYL6;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE FAS LIGAND.  
 GN PT-FASL OR CM-FASL OR RM-FASL.  
 OS Macaca nemestrina (Pig-tailed macaque),  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Macaca.  
 OX NCBI\_TaxID-9545, 9541, 9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY;  
 RA Kirii Y., Inoue T., Yoshino K.;  
 RT "Pig-tailed monkey Fas ligand mRNA, complete cds."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;  
 RA Kirii Y., Inoue T., Yoshino K.;  
 RT "Cynomolgus monkey Fas ligand mRNA, complete cds."  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;

RA Kirii Y., Inoue T., Yoshino K.;  
RT \*Rhesus monkey Fas ligand mRNA, complete cds.\*;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB035140; BAA90296.1; -  
DR EMBL; AB035138; BAA90294.1; -  
DR EMBL; AB035139; BAA90295.1; -  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_abc; 1.  
DR ProDom; PD008600; TNF\_5; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS0049; TNF\_2; 1.  
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 11.0%; Score 186; DB 6; Length 280;  
Best Local Similarity 22.1%; Pred. No. 7.4e-09;  
Matches 69; Conservative 44; Mismatches 103; Indels 96; Gaps 11;

QY 22 PGAPHEGLHAPPPAP-----HPPAASRS-----MFVALLGLGLGOVCS 63  
DB 45 PPPPPPPPLPPPPSPPLPLPLPLPKKRGHSTGLCLLVFMFVVALVGLGLG----- 99  
QY 64 VALFFYFRAQMDPNRISEDGTHCIYRILRLHENADPQDTTLESQDTKLIPDSRRIKQAF 123  
DB 100 ---MFOLFHLQ-----KELAELESTSQKHTA----- 123  
QY 124 QGAVQKELQHVIGSQHRAEKAMVDGSLDLAKRSKLEAQPFAHLT--INATDIPSGSHK 181  
DB 124 -SSLEKQIGH-----PSPPEKKEQKVAHLTKGPNRSRMP----- 158  
QY 182 VLSLWYHHRGNAKISNMTFSGKLVNODGFYLYANICFRHETSGDLATEYLQLMVY 241  
DB 159 ---LEWEDYIGVLLSGVKYKGLVINETGLYFYVSKYFR-----GQSCIN-LPLSHK 209  
QY 242 VTKTSIKPSSHTLMKGGSTKYWSGNSEPHFYISINVGFFKLRSGEISIEVSNPSLLDP 301  
DB 210 VYMRNSKYPQDLVMEGKMSYCT-TGOMWAHSSYLGAVENTLSADHLVYVNSLSLVNF 268  
QY 302 DQDATYFGAFKV 313  
DB 269 EESQTFFGLYKL 280

RESULT 13  
Q9BDM5

Q9BDM5 PRELIMINARY; PRT; 280 AA.  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE FAS ANTIGEN CD95.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21383618; PubMed-11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate  
RT Fas/Fas-ligand and co-stimulatory molecules.";  
RL Immunogenetics 53:315-328(2001).  
DR EMBL; AF344856; AAK37539.1; -  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR002965; P-rich\_extensn.  
DR InterPro; IPR003263; TNF\_5.

DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01217; PRICEXTENS.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_abc; 1.  
DR ProDom; PD008600; TNF\_5; 1.  
DR SMART; SM00207; TNF; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS0049; TNF\_2; 1.  
SQ SEQUENCE 280 AA; 31377 MW; 729EA61436F2D398 CRC64;

Query Match 10.9%; Score 184.5; DB 6; Length 280;  
Best Local Similarity 22.4%; Pred. No. 1e-08;  
Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

QY 22 PGAPHEGLHAPPPAPPPHAPP-----AASRS-----MFVALLGLGLGOVVC 62  
DB 46 PPPPPPPPLPPPPPPPLPLPLPKKRGHSTGLCLLVFMFVVALVGLGLG----- 99  
QY 63 SVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADPQDTTLESQDTKLIPDSRRIKOA 122  
DB 100 ---MFOLFHLQ-----KELAELESTSQKHTA----- 123  
QY 123 FQAVQKELQHVIGSQHRAEKAMVDGSLDLAKRSKLEAQPFAHLT--INATDIPSGSH 180  
DB 124 -SSLEKQIGH-----PSPPEKKEQKVAHLTKGPNRSRMP----- 158  
QY 181 KVSLSWYHHRGNAKISNMTFSGKLVNODGFYLYANICFRHETSGDLATEYLQLMVY 240  
DB 159 ---LEWEDYIGVLLSGVKYKGLVINETGLYFYVSKYFR-----GQSCIN-LPLSH 208  
QY 241 VYTKTSIKPSSHTLMKGGSTKYWSGNSEPHFYISINVGFFKLRSGEISIEVSNPSLLD 300  
DB 209 KYMRNSKYPQDLVMEGKMSYCT-TGOMWAHSSYLGAVENTLSADHLVYVNSLSLVN 267  
QY 301 PDQATYFGAFKV 313  
DB 268 EESQTFFGLYKL 280

RESULT 14  
Q9BDN1

Q9BDN1 PRELIMINARY; PRT; 280 AA.  
AC Q9BDN1  
DT 01-JUN-2001 (TRENBLrel. 17, Created)  
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE CD95L PROTEIN.  
GN CD95L.  
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9531;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21383618; PubMed-11491535;  
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,  
RA Weiss W.R., Ansari A.A.;  
RT "Cloning, sequencing, and homology analysis of nonhuman primate  
RT Fas/Fas-ligand and co-stimulatory molecules.";  
RL Immunogenetics 53:315-328(2001).  
DR EMBL; AF344847; AAK37606.1; -  
DR HSSP; P01375; 4TSV.  
DR InterPro; IPR002965; P-rich\_extensn.  
DR InterPro; IPR003263; TNF\_5.  
DR InterPro; IPR003636; TNF\_abc.  
DR InterPro; IPR000478; TNF\_family.  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01217; PRICEXTENS.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR ProDom; PD002012; TNF\_abc; 1.

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DR ProDom; PD008600; TNE_5; 1.
DR SMART; SM00207; TNE_1; 1.
DR PROSITE; PS00251; TNE_1; 1.
DR PROSITE; PS00049; TNE_2; 1.
SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;

Query Match      10.8%; Score 182.5; DB 6; Length 280;
Best Local Similarity 22.4%; Pred. No. 1.5e-08;
Matches 70; Conservative 44; Mismatches 100; Indels 99; Gaps 12;

QY 22 PGAPHEGLHAPPPAPAPAPP-----AASRS-----MFVALLGLGLGVVC 62
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123 FOGAVOKELQHVGSQHIAERAKAMVDGSLDLAKRSKLEAQPFAHLT--INATDIPSGSH 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 124 --SSLEKQIGH-----PSPPEKKEQKRVKVAHLTGKPNRSMP----- 158

QY 181 KYLSLSWYHDSWAKISNNTFNGKLIYNQDGFYIYANICFRHHTSGDLATEYQLQMW 240
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 ----LEWEDTYGIVLLSGVKYKGGIVINETGLYFYVKYFR-----GQSCTN-LPLSH 208

QY 241 YVTKTSIKIPSHSTLMKSGTKYWSNSEFHYFSINVGFFKLRSGEEISIEVSNPSLLD 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 209 KYIMRNKYPQDLVMMEGKMSYCT-TGQMAHSSYLGAVFNLSTPDHLYVNVVSELV 267

QY 301 PQDATYFGAFKV 313
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Db 268 FEESQTFGLYKL 280

RESULT 15
Q9BDN3 PRELIMINARY; PRT; 261 AA.
AC Q9BDN3;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CD154 PROTEIN.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
NCBI_TaxID=9483;
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RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344844; RAK37603.1;
DR HSSP; P29965; IALX.
DR InterPro; IPR003263; TNE_5.
DR InterPro; IPR000478; TNE_family.
DR Pfam; PF00229; TNE_1.
DR ProDom; PD008600; TNE_5; 1.
DR SMART; SM00207; TNE_1.
DR PROSITE; PS00251; TNE_1; 1.
DR PROSITE; PS00049; TNE_2; 1.
SQ SEQUENCE 261 AA; 29360 MW; 10CA588D923754EB CRC64;

Query Match      10.1%; Score 169.5; DB 6; Length 261;
Best Local Similarity 24.6%; Pred. No. 2.1e-07;
Matches 71; Conservative 55; Mismatches 120; Indels 43; Gaps 15;

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Db 8 PVPRSAATGPPVSMKIFMYLLTVFLITQMGSALEAVYLHRRLD--KIEDE-----R 57

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Db 58 NLHEDFVFMKTIQRCNTGERSLSLLNCEIEIKSQFEGFV-KDIM-----LNKEKKEN 109
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QY 150 SWLDLAKRSKLEAQPFAHLTINATDIPSGSHKVSLSWYHDSWAKISN--WTFSSNGK-L 206
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 110 SF-EMOKGQD-NPQIAAHVISEAS-----SKTTSVLQW-AERGIYPMNSNLTLENGKQL 161
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QY 207 IVNODGFYIYANICFRHHTSGDLATEYQLQMWVYVTKTSIKIPS--SHTLMKGGSTKYW 264
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 162 TVARQGLIYIYQVTFCSNREASSQAP-----FIASCLKPPNPFERILLRAANTH-- 212
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QY 265 SGNSEFHYFSINVGFFKLRSGEEISIEVSNPSLLDQDQDATYFGAFKV 313
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Db 213 SSAKPCGQSIHLGGIFELQPGASVFNVTDPQSVSHGTGFTSGLLKL 261

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Search completed: October 10, 2002, 16:03:00  
Job time : 107.166 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 38.1928 Seconds  
(without alignments)  
202.732 Million cell updates/sec

Title: US-09-787-126-2  
Perfect score: 1685  
Sequence: 1 MRRASRDYTKYLRGSEEMGG.....LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Aligned: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description       |
|------------|--------|-------------|--------|----|-------------------|
| 1          | 1685   | 100.0       | 317    | 3  | US-08-996-139-13  |
| 2          | 1685   | 100.0       | 317    | 4  | US-08-995-659-13  |
| 3          | 1685   | 100.0       | 317    | 4  | US-09-215-649A-13 |
| 4          | 1685   | 100.0       | 317    | 4  | US-09-052-521C-4  |
| 5          | 1417.5 | 84.1        | 316    | 2  | US-08-842-842-7   |
| 6          | 1417.5 | 84.1        | 316    | 4  | US-08-989-362-2   |
| 7          | 1417.5 | 84.1        | 316    | 4  | US-09-052-521C-2  |
| 8          | 1326.5 | 78.7        | 294    | 3  | US-08-996-139-11  |
| 9          | 1326.5 | 78.7        | 294    | 4  | US-08-995-659-11  |
| 10         | 1326.5 | 78.7        | 294    | 4  | US-09-215-649A-11 |
| 11         | 251.5  | 14.9        | 279    | 4  | US-09-072-993C-3  |
| 12         | 251.5  | 14.9        | 281    | 1  | US-08-670-354-2   |
| 13         | 251.5  | 14.9        | 281    | 3  | US-08-584-031-1   |
| 14         | 251.5  | 14.9        | 281    | 3  | US-08-780-496-1   |
| 15         | 251.5  | 14.9        | 281    | 4  | US-08-883-086-10  |
| 16         | 251.5  | 14.9        | 281    | 4  | US-09-320-424-2   |
| 17         | 251.5  | 14.9        | 281    | 4  | US-09-333-593A-6  |
| 18         | 251.5  | 14.9        | 281    | 5  | PCT-US96-10895-2  |
| 19         | 248    | 14.7        | 291    | 1  | US-08-670-354-6   |
| 20         | 248    | 14.7        | 291    | 4  | US-09-320-424-6   |
| 21         | 248    | 14.7        | 291    | 5  | PCT-US96-10895-6  |
| 22         | 236.5  | 14.0        | 253    | 4  | US-09-320-424-11  |
| 23         | 236.5  | 14.0        | 256    | 4  | US-09-320-424-13  |
| 24         | 231.5  | 13.7        | 177    | 4  | US-09-105-343A-7  |
| 25         | 226.5  | 13.4        | 183    | 4  | US-09-105-343A-8  |
| 26         | 189    | 11.2        | 281    | 2  | US-08-810-453-2   |
| 27         | 189    | 11.2        | 281    | 3  | US-08-815-190A-2  |

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| 28 | 189   | 11.2 | 281 | 4 | US-09-290-640-25 |
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| 31 | 189   | 11.2 | 281 | 4 | US-08-339-214-30 |
| 32 | 189   | 11.2 | 281 | 5 | PCT-US95-00362-2 |
| 33 | 184.5 | 10.9 | 279 | 4 | US-08-339-214-24 |
| 34 | 184.5 | 10.9 | 279 | 4 | US-08-339-214-32 |
| 35 | 184.5 | 10.9 | 279 | 5 | PCT-US95-00362-5 |
| 36 | 175.5 | 10.4 | 278 | 4 | US-08-339-214-16 |
| 37 | 175.5 | 10.4 | 278 | 4 | US-08-339-214-26 |
| 38 | 164.5 | 9.8  | 376 | 3 | US-08-751-512-8  |
| 39 | 158.5 | 9.4  | 261 | 1 | US-07-940-605A-2 |
| 40 | 158.5 | 9.4  | 261 | 1 | US-08-184-422-8  |
| 41 | 158.5 | 9.4  | 261 | 1 | US-08-360-933A-2 |
| 42 | 158.5 | 9.4  | 261 | 1 | US-08-446-933-4  |
| 43 | 158.5 | 9.4  | 261 | 2 | US-08-431-055-4  |
| 44 | 158.5 | 9.4  | 261 | 2 | US-08-690-096-2  |
| 45 | 158.5 | 9.4  | 261 | 2 | US-08-249-189-12 |

## ALIGNMENTS

RESULT 1  
US-08-996-139-13  
; Sequence 13, Application US/08996139  
; Patent No. 6017729  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent  
; APPLICANT: Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,139  
; FILING DATE: 22 DECEMBER 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/064,671  
; FILING DATE: 14 OCTOBER 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2851-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 317 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-996-139-13

|                   |
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| Sequence 25, Appl |
| Sequence 3, Appl  |
| Sequence 8, Appl  |
| Sequence 30, Appl |
| Sequence 2, Appl  |
| Sequence 24, Appl |
| Sequence 32, Appl |
| Sequence 5, Appl  |
| Sequence 16, Appl |
| Sequence 26, Appl |
| Sequence 8, Appl  |
| Sequence 2, Appl  |
| Sequence 8, Appl  |
| Sequence 2, Appl  |
| Sequence 4, Appl  |
| Sequence 2, Appl  |
| Sequence 12, Appl |

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Query Match      100.0%; Score 1685; DB 3; Length 317;
Best Local Similarity 100.0%; Pred. No. 9.8e-164;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB   61 VCSVALFFYFRAQMDPNRISDGTCHCIYIRLRLHENADFQDTTLESQDTKLIPDSRRIK 120

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DB   121 QAFQAGVQKELQHIVGSOIHIAEAKWVDGSWLDAKRSKLEAQPTFAHLTNATIDIPSGSH 180

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DB   181 KVSLSSTHWDHGWAKISNMTFSNGKLIYNODGFYYLYANICFRHHETSGDLATEYLQLMV 240

QY   241 YVTKTSIKIPSSHTLMKGSGKYNSGNSEFHFIYSINVGFFKLRSGEEISIEVSNPSLLD 300
DB   241 YVTKTSIKIPSSHTLMKGSGKYNSGNSEFHFIYSINVGFFKLRSGEEISIEVSNPSLLD 300

QY   301 PDQDATYFGAFKVRDID 317
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RESULT 2
US-08-995-659-13
: Sequence 13, Application US/08995659
: Patent No. 6242213
: GENERAL INFORMATION:
: APPLICANT: Anderson, Dirk M.
: APPLICANT: Galibert, Laurent
: APPLICANT: Maraskovsky, Eugene
: TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation, Law Department
: STREET: 51 University Street
: CITY: Seattle
: STATE: WA
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Power Macintosh
: OPERATING SYSTEM: Apple Operating System 7.5.5
: SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/995,659
: FILING DATE: 22 DECEMBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 60/064,671
: FILING DATE: 14 OCTOBER 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/813,509
: FILING DATE: 07 MARCH 1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/772,330
: FILING DATE: 23 DECEMBER 1996
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,693
: REFERENCE/DOCKET NUMBER: 2852-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430

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REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 317 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-215-649A-13

Query Match      100.0%; Score 1685; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 9.8e-164;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MRRASRDYTKYLGRSEMGPGAPHEGPHLHAPPAPHPAPHPAASRSMFVALLGLGLGV 60
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61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSRRIK 120
|||||
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121 QAFQAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
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|||||

241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYQINVGFFKLRSGEISIEVSNPSLLD 300
|||||
241 YVTKTSIKIPSSHTLMKGGSTKYWSGSEFFHYQINVGFFKLRSGEISIEVSNPSLLD 300
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301 PQDATYFGAFKVRDID 317
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301 PQDATYFGAFKVRDID 317
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RESULT 5
US-08-842-842-7
Sequence 7, Application US/08842842
Patent No. 5843678
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Behavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91230-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,842
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-451
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-842-842-7

Query Match      84.1%; Score 1417.5; DB 2; Length 316;
Best Local Similarity 84.3%; Pred. No. 1.9e-136;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

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60 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSRRIK 119
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119 QAFQAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 178
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119 QAFQAVOKELQHVGSQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSH 178
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180 HKVSLSSWYHDSRWAKISNMTFSGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLMV 239
|||||
180 HKVSLSSWYHDSRWAKISNMTFSGKLIYNQDGFYLYANICFRHHETSGDLATEYLQLMV 239
|||||
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Db 179 HKVTLSWYHGRGAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLM 238
Qy 240 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 299
Db 239 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 298
Qy 300 DPQDQATYFGAFKVRDID 317
Db 299 DPQDQATYFGAFKVRDID 316

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RESULT 6
US-08-989-362-2
; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/08/989,362
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 56
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-989-362-2

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Query Match 84.1%; Score 1417.5; DB 4; Length 316;
Best Local Similarity 84.3%; Pred. No. 1.9e-136;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 59
Db 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 60

Qy 60 VVCSVALFFYFRAQMDPNRISEDTGHCYRILRLHENAADFQDTLESODTKLIPDSCRRI 119
Db 61 VVCSIALFLYFRAQMDPNRISEDTGHCYRILRLHENAAGLQDSTLESDT--LPDSCRRI 118

Qy 120 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKSKLEAQPFAHLLTNATDIPSGS 179
Db 119 KOAFQAVQKELQHVGPQRFSGAPAMMEGSLDLVAQKGPFAHLLTNAAISIPSGS 178

Qy 180 HKVSLSSWYHGRGAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGDLATEYLQLM 239
Db 179 HKVTLSSWYHGRGAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLM 238

Qy 240 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 299
Db 239 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 298

Qy 300 DPQDQATYFGAFKVRDID 317
Db 299 DPQDQATYFGAFKVRDID 316

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Db 179 HKVTLSWYHGRGAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLM 238
Qy 240 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 299
Db 239 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 298
Qy 300 DPQDQATYFGAFKVRDID 317
Db 299 DPQDQATYFGAFKVRDID 316

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RESULT 7
US-09-052-521C-2
; Sequence 2, Application US/09052521C
; Patent No. 6316408
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: Osteoprotegerin Binding Proteins and Receptors
; FILE REFERENCE: A-451Brv
; CURRENT APPLICATION NUMBER: US/09/052,521C
; CURRENT FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 08/880,855
; PRIOR FILING DATE: 1997-06-23
; PRIOR APPLICATION NUMBER: 08/842,842
; PRIOR FILING DATE: 1997-04-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Mouse
; US-09-052-521C-2

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Query Match 84.1%; Score 1417.5; DB 4; Length 316;
Best Local Similarity 84.3%; Pred. No. 1.9e-136;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

Qy 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 59
Db 1 MRRASRDYTKYLRGSEEMGGGAPHEGLH-APPPHAPHOPPAASRSFMFALLGLGLGQ 60

Qy 60 VVCSVALFFYFRAQMDPNRISEDTGHCYRILRLHENAADFQDTLESODTKLIPDSCRRI 119
Db 61 VVCSIALFLYFRAQMDPNRISEDTGHCYRILRLHENAAGLQDSTLESDT--LPDSCRRI 118

Qy 120 KOAFQAVQKELQHVGSQHIRAEKAMVDGSLDLAKSKLEAQPFAHLLTNATDIPSGS 179
Db 119 KOAFQAVQKELQHVGPQRFSGAPAMMEGSLDLVAQKGPFAHLLTNAAISIPSGS 178

Qy 180 HKVSLSSWYHGRGAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGDLATEYLQLM 239
Db 179 HKVTLSSWYHGRGAKISNMTLSNGKLRVNDGFYLYANICFRHHETSGSVPTDYQLM 238

Qy 240 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 299
Db 239 VYVTKTSIKIPSSHTLMKGGSTKWSGNSSEPHFYSINVGFFKLRSGEIEISIEVSNPSLL 298

Qy 300 DPQDQATYFGAFKVRDID 317
Db 299 DPQDQATYFGAFKVRDID 316

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RESULT 8
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19

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CLASSIFICATION:  
PRIOR APPLICATION DATA: USN 60/064,671  
APPLICATION NUMBER: USN 60/064,671  
FILING DATE: 14 OCTOBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA: USN 08/813,509  
APPLICATION NUMBER: USN 08/813,509  
FILING DATE: 07 MARCH 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA: USN 08/772,330  
APPLICATION NUMBER: USN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2852-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

GENERAL: 254 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PDB: 1S-08-995-659-11

|    | Query Match           | 78.7%;   | Score 1326.5;       | DB 4;     | Length 294; |
|----|-----------------------|--|---------------------|-----------|-------------|
|    | Best Local Similarity | 84.5%;   | Pred. No. 3.2e-121; |           |             |
|    | Matches 250;          | Conservative 16;   | Mismatches 27;      | Indels 3; | Gaps        |
| QY | 23                    | GAPHEGPLH-APPHPAPHPPAASRMFVALLGLGLGVQVCVSVALFFYFRAQMDPNRISE 81   |                     |           |             |
| Db | 1                     | GVPEHGLHPAPSAPAPAPAPPPAASRMFTALLGLGLGVQVCSTALFFYFRAQMDPNRISE 60  |                     |           |             |
| QY | 82                    | DSTFCYIRILRLHENADFDTLLESOOTKLIPDSCRRIKAQFOGAVOKELQHLIVGSOHIR 141 |                     |           |             |
| Db | 61                    | DSTHCFIRILRLHENADLDQSTLESEDT--LPDSCRMRKAQFOGAVOKELQHLIVGPQRS 118 |                     |           |             |
| QY | 142                   | AEKAMVDGSLDLAKRSKLEAOPFAHLTTNADTIPSGSHKVSLSWYHDSGAKINSMTFF 201   |                     |           |             |
| Db | 119                   | GAPAMEGSWLDYAQRCKTEAOPFAHLTTNAAISIPSGSHKVTLSWYHDSGAKINSMTL 178   |                     |           |             |
| QY | 202                   | SNCKLIVNODGFYLLYANICFRHHETSGDLATEYLQMLVYVTKTSIKIPSSHTLMKGGST 261 |                     |           |             |
| Db | 179                   | SNCKLRVNDGGFYLLYANICFRHHETSGSVPTDYLOLMVYVTKTSIKIPSSHNLMKGGST 238 |                     |           |             |

|   |     |   |     |
|---|-----|---|-----|
| Oy  | 262 | KWMSGNSEPHFYSINVGGFFKLRSGEELISIEVSNPSLLDPDQDATYFGAFKVVDID | 317 |
|   |     | :           :           :           :                     |     |
| Db  | 239 | KWMSGNSEFHYSINVGGFFKLRAGEELISIQVSNPSLLDPDQDATYFGAFKVQIID  | 294 |
| <br>RESULT 10<br>US-09-215-649A-11<br>: Sequence 11, Application US/09215649A |     |   |     |



Patent No. 6271349  
 GENERAL INFORMATION:  
 APPLICANT: Anderson, Dirk M.  
 Calibert, Laurent  
 Maraskovsky, Eugene  
 TITLE OF INVENTION: Receptor Activator of NF-kappaB  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Immunex Corporation, Law Department  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Power Macintosh  
 OPERATING SYSTEM: Apple Operating System 7.5.5  
 SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/215,649A  
 FILING DATE: 17-Dec-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/996,139  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: USSN 08/813,509  
 FILING DATE: 07 MARCH 1997  
 APPLICATION NUMBER: USSN 08/772,330  
 FILING DATE: 23 DECEMBER 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Perkins, Patricia Anne  
 REGISTRATION NUMBER: 34,693  
 REFERENCE/DOCKET NUMBER: 2851-A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206)587-0430  
 TELEFAX: (206)233-0644  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 294 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Sequence 3, Application US/09072993C  
 Patent No. 6346388  
 GENERAL INFORMATION:  
 APPLICANT: Michael R. Brigham-Burke  
 APPLICANT: Peter R. Young  
 TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND  
 TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRI AND TR2  
 FILE REFERENCE: GH-50030  
 CURRENT APPLICATION NUMBER: US/09/072,993C  
 CURRENT FILING DATE: 1998-05-06  
 PRIOR APPLICATION NUMBER: 60/055,513  
 PRIOR FILING DATE: 1997-08-13  
 PRIOR APPLICATION NUMBER: 60/056,980  
 PRIOR FILING DATE: 1997-08-26  
 PRIOR APPLICATION NUMBER: 60/057,550  
 PRIOR FILING DATE: 1997-08-29  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 3  
 LENGTH: 279  
 TYPE: PRT  
 ORGANISM: HOMO SAPIENS  
 US-09-072-993C-3

Query Match 14.9%; Score 251.5; DB 4; Length 279;  
 Best Local Similarity 24.1%; Pred. No. 1.4e-17;  
 Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;  
 QY 42 PAASRSMFVALLGLGVGVCSVALFFYFRAQMD--PNRISEDTGHCYRILRLHENA 99  
 DB 8 PSLGTCVLIVITVLLQSLCAVAVYVYFTNELKQMDKYSKGIACF-----LKED--- 59  
 QY 100 QDTTLESQTKLPDSCRRIKQAFQVQKELQHVGSQHIRAEKAMVDGSGWLDLAKRSK 159  
 DB 60 -DSYWDPNDESMNSPCQVKN-----QLRQLVKRMILRTSEETI-----STVQEKQ 105  
 QY 160 LEAQPF-----AHLT-----INATDIPSGSHKVS-----SSMYHDR-GWAKISNM 199  
 DB 106 QNISPLVRERGPQVAAHITGTGRSNTLSSPNSKNEKALGRKINSWESSRSHSFLSNL 165  
 QY 200 TFSNGLIVNQDGFYLYANICFRHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259  
 DB 166 HLRNGELVHEKGFYIYQTVYRFOEIKENTKNDQMYYIKYT-SYPDPILLMKA 224  
 QY 260 STKWSGSEFHYISINVGFFKLRSGEISIEVSNPSLLDPDQDATYFGAFKV 313  
 DB 225 RNSCNSKDAEYGLYSYIQQGIFELKENDRIFVSVTNEHLIDMDREASFFGAFV 278

RESULT 12  
 US-08-670-354-2  
 Sequence 2, Application US/08670354  
 Patent No. 5763223  
 GENERAL INFORMATION:  
 APPLICANT: Steven R. Wiley and  
 APPLICANT: Raymond G. Goodwin  
 TITLE OF INVENTION: Cytokine that Induces Apoptosis  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
 STREET: 51 University Street  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98101  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Apple 7.5.2  
 SOFTWARE: Microsoft Word, Version 6.0.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/670,354  
 FILING DATE: 25-JUN-1996

Query Match 78.7%; Score 1326.5; DB 4; Length 294;  
 Best Local Similarity 84.5%; Pred. No. 3.2e-127;  
 Matches 250; Conservative 16; Mismatches 27; Indels 3; Gaps 2;  
 DB 23 GAPHEGLR-APPPAPHOPPAASRSMFVALLGLGVGVCSVALFFYFRAQMDPNRISE 81  
 QY 1 GVPHEGLHPAPAPAPAPPAASRSMFVALLGLGVGVCSIALFLYFRAQMDPNRISE 60  
 DB 82 DGTCHYRILRLHENAQDTTLESQTKLPDSCRRIKQAFQVQKELQHVGSQHIR 141  
 DB 61 DSTHCFYRILRLHENAQLDQSTLESDT--LPDSCRMRKQAFQVQKELQHVGPQRS 118  
 QY 142 AEKAMVDGSHLDLAKRSKLEAQPFALHTINATDIPSGSHKVSLSYVHGRGWAKISNM 201  
 DB 119 GAPAMEGSWLDVAQRKPEAQPFALHTINAAIPSGSHKVSLSYVHGRGWAKISNM 178  
 QY 202 SNGLIVNQDGFYLYANICFRHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 261  
 DB 179 SNGLRVNQDGFYLYANICFRHETSGSVPTDYQLQLMVYVTKTSIKIPSSHNLKGG 238  
 QY 262 KYWSGSEFHYISINVGFFKLRSGEISIEVSNPSLLDPDQDATYFGAFKV 317  
 DB 239 KNWSGSEFHYISINVGFFKLRSGEISIEVSNPSLLDPDQDATYFGAFKV 294

RESULT 11  
 US-09-072-993C-3

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DB      10 PSLGQTCVLIVFTVLLQSCLCVAVYVYFYNELKQMOKDYKSRSKIACF-----LKED--- 61
QY      100 QDTTLESQDKLIPDSCKRIKAQFOGAVQKELOHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
DB      62 -DSYWDPNDEESMNSPCWQVKW-----QLRQLVRKMILRTSEETI-----STVOEKQ 107
QY      160 LEAQPF-----AHLT-----INATDIPSGSHKVSU-----SSWYHDR-GWAKISNM 199
DB      108 QNISPLVRRGPORVAAHITGTGRSNTLSSPNSKKKALGRKINGSWESSRSGHSFLSNL 167
QY      200 TFSNGKLIVNOCGFYYLYANICFRHHETSGLATEYLQLMVVYTKTSIKIPSSHLMKGG 259
DB      168 HLRNGELVIEHGFFYYIYSQTFRFOEIKEKENTNDKMWQVIYKYT-SYPDPILLMSKA 226
QY      260 STKYNSGNSEFHFIYINVGGFFKLRSGEEISIEVSNPSLLDDPOODATYFGAFKV 313
DB      227 RNSCWSKDAEYGLYSIQOGIFPELKENDRFVSVTNEHLIDMDHEASFFCAFLV 280

RESULT 14
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-780-496-1

Query Match          14.9%; Score 251.5; DB 3; Length 281;
Best Local Similarity 24.1%; Pred. No. 1.4e-17;
Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

QY      42 PAASRMFEVALIGLGIOGVYCSVALFFVFQAQMD--PNRISGDGTHCIYRILRLHENADF 99
DB      10 PSLGQTCVLIVFTVLLQSCLCVAVYVYFYNELKQMOKDYKSRSKIACF-----LKED--- 61
QY      100 QDTTLESQDKLIPDSCKRIKAQFOGAVQKELOHIVGSQHIRAEKAMVDGSWLDLAKRSK 159
DB      62 -DSYWDPNDEESMNSPCWQVKW-----QLRQLVRKMILRTSEETI-----STVOEKQ 107
QY      160 LEAQPF-----AHLT-----INATDIPSGSHKVSU-----SSWYHDR-GWAKISNM 199
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Db 108 QNISPLVREGRQVAAHITCTGRKSNLTSSPNKNEKALGRKINSWESSRSGHSLNL 167  
 Qy 200 TFSNGKLIIVNDGGYLYANICFRHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259  
 Db 168 HLRNGELVHEKGFYIYSQYFRFOEEIKENTKNDKQMVQYIYKYT-SYDPDILLMKSA 226  
 Qy 260 STKYWSGNSEPHFYISINVGGFKLRSGEISIEVSNPSLLDPDQDATYFGAFKV 313  
 Db 227 RNSCWSKDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280

RESULT 15

US-08-883-086-10  
 ; Sequence 10, Application US/08883086  
 ; Patent No. 6171787

; GENERAL INFORMATION:  
 ; APPLICANT: WILEY, STEVEN  
 ; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL  
 ; TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Addott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/883,086

FILING DATE:  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:

FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Foremski, Priscilla E.  
 REGISTRATION NUMBER: 33,207  
 REFERENCE/DOCKET NUMBER: 6134.US.01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847-937-0378  
 TELEFAX: 847-938-2623  
 TELEX:

INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 281 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 6171787e  
 US-08-883-086-10

Query Match 14.9%; Score 251.5; DB 4; Length 281;  
 Best Local Similarity 24.1%; Pred. No. 1.4e-17;  
 Matches 71; Conservative 61; Mismatches 117; Indels 45; Gaps 10;

Qy 42 PAASRSMFVALLGLGVGVCSVALFFYFPAQMD--PNRISDGTGHCYIRILRLHENADF 99  
 Db 10 PSLGQTCVLIVFTVLLQSLCVAVYVYTNELKQMDKYSKGTACF-----LKED--- 61  
 Qy 100 QDTLLESQTKLIPDSCKRIKQAFQAVOKELQHVGSQHIRAEKAWVDGSLDLAKRSK 159  
 Db 62 -DSYNDPNDSESMNSPCWQVKW-----QLRLVRKMLRTSETI-----STVQEKQ 107  
 Qy 160 LEAQP-----AHLT-----INATDIPSGSHKVS-----SSWYHDR-GWAKISNM 199  
 Db 108 QNISPLVREGRQVAAHITCTGRKSNLTSSPNKNEKALGRKINSWESSRSGHSLNL 167  
 Qy 200 TFSNGKLIIVNDGGYLYANICFRHETSGDLATEYLQLMVYVTKTSIKIPSSHTLMKGG 259

Db 168 HLRNGELVHEKGFYIYSQYFRFOEEIKENTKNDKQMVQYIYKYT-SYDPDILLMKSA 226  
 Qy 260 STKYWSGNSEPHFYISINVGGFKLRSGEISIEVSNPSLLDPDQDATYFGAFKV 313  
 Db 227 RNSCWSKDAEGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 280

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

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Title: us-09-787-126-34

Perfect score: 74

Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 74    | 100.0       | 15     | AA06310  | Tetanus toxin epit |
| 2          | 74    | 100.0       | 15     | AAW35506 | Universal T-cell e |
| 3          | 74    | 100.0       | 15     | AAW11505 | Tetanus toxoid uni |
| 4          | 74    | 100.0       | 15     | AAW67033 | Tetanus toxin frag |
| 5          | 74    | 100.0       | 15     | AAW71321 | Universal helper T |
| 6          | 74    | 100.0       | 15     | AAW04051 | T-helper epitope f |
| 7          | 74    | 100.0       | 15     | AAW67578 | T-cell epitope pep |
| 8          | 74    | 100.0       | 15     | AAW73220 | Tetanus toxoid epi |
| 9          | 74    | 100.0       | 15     | AAW45511 | Tetanus P2 epitope |
| 10         | 74    | 100.0       | 15     | AAW82637 | Tetanus toxoid T c |
| 11         | 74    | 100.0       | 15     | AAW92625 | Foreign epitope P2 |

|    |    |       |    |    |          |                    |
|----|----|-------|----|----|----------|--------------------|
| 12 | 74 | 100.0 | 15 | 21 | AAW84427 | Amino acid sequenc |
| 13 | 74 | 100.0 | 15 | 21 | AAW70300 | Clostridium tetani |
| 14 | 74 | 100.0 | 15 | 21 | AAW44763 | Tetanus toxoid pro |
| 15 | 74 | 100.0 | 15 | 22 | AAE11763 | Clostridium tetani |
| 16 | 74 | 100.0 | 15 | 22 | AAW99515 | Vaccine related MH |
| 17 | 74 | 100.0 | 15 | 22 | AAW85701 | Amino acid sequenc |
| 18 | 74 | 100.0 | 15 | 22 | AAW8451  | Wild-type TT830 (t |
| 19 | 74 | 100.0 | 15 | 22 | AAW61956 | Tetanus toxoid uni |
| 20 | 74 | 100.0 | 15 | 22 | AAW20143 | Tetanus toxin T-ce |
| 21 | 74 | 100.0 | 15 | 22 | AAW68636 | HER-2 B cell pepti |
| 22 | 74 | 100.0 | 15 | 22 | AAW46172 | Tetanus toxoid TT8 |
| 23 | 74 | 100.0 | 15 | 22 | AAW49071 | Tetanus toxoid TT  |
| 24 | 74 | 100.0 | 16 | 18 | AAW33445 | T-cell stimulatory |
| 25 | 74 | 100.0 | 16 | 20 | AAW29705 | Clostridium tetani |
| 26 | 74 | 100.0 | 17 | 15 | AAW62692 | Helper T cell epit |
| 27 | 74 | 100.0 | 17 | 16 | AAW82573 | Tetanus toxin help |
| 28 | 74 | 100.0 | 17 | 17 | AAW05599 | Tetanus toxin help |
| 29 | 74 | 100.0 | 17 | 17 | AAW8395  | T-cell antigen TT2 |
| 30 | 74 | 100.0 | 17 | 21 | AAW99274 | HLA class II bindi |
| 31 | 74 | 100.0 | 17 | 21 | AAW80056 | Pathogen derived T |
| 32 | 74 | 100.0 | 17 | 21 | AAW54539 | T helper cell (Th) |
| 33 | 74 | 100.0 | 17 | 21 | AAW58768 | Unidentified pepti |
| 34 | 74 | 100.0 | 17 | 22 | AAW9516  | Vaccine related MH |
| 35 | 74 | 100.0 | 17 | 22 | AAW62904 | Amino acid residue |
| 36 | 74 | 100.0 | 17 | 22 | AAW84435 | Amino acid sequenc |
| 37 | 74 | 100.0 | 17 | 22 | AAW30941 | Amino acid sequenc |
| 38 | 74 | 100.0 | 17 | 22 | AAW31029 | Antigenic fragment |
| 39 | 74 | 100.0 | 17 | 22 | AAW31118 | Antigenic fragment |
| 40 | 74 | 100.0 | 17 | 22 | AAW15589 | Peptide 5 for pept |
| 41 | 74 | 100.0 | 18 | 20 | AAW26607 | HIV-derived lipope |
| 42 | 74 | 100.0 | 19 | 21 | AAW99055 | HLA class II bindi |
| 43 | 74 | 100.0 | 19 | 22 | AAW9517  | Vaccine related MH |
| 44 | 74 | 100.0 | 22 | 22 | AAW46175 | Tetanus toxoid 830 |
| 45 | 74 | 100.0 | 22 | 22 | AAW46178 | Tetanus toxoid 830 |

## ALIGNMENTS

RESULT 1  
AAW06310  
ID AAR06310 standard; protein; 15 AA.  
XX  
AC AAR06310;  
XX  
DT 04-DEC-1990 (first entry)  
XX  
DE Tetanus toxin epitope.  
XX  
KW Tetanus toxin; vaccine; major histocompatibility complex; MHC;  
KW antimalarial.  
XX  
OS Synthetic.  
XX  
PN EP378881-A.  
XX  
PD 25-JUL-1990.  
XX  
PF 27-DEC-1989; 89EP-0203318.  
XX  
PR 16-NOV-1989; 89IT-0022409.  
PR 17-JAN-1989; 89IT-0019110.  
XX  
(ENIE ) ENIRICERHE SPA.  
XX  
PI Pessi A, Bianchi E, Verdini AS, Corradin G;  
XX  
DR WPI; 1990-225582/30.  
XX  
PT Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used  
PT as universal carriers for prepn. of immunogenic conjugate(s) for  
PT use as vaccines.  
XX

PS Claim 1; Page 17; 20pp; English.

XX Epitopic peptides may be used with synthetic haptens derived from  
CC a pathogen to generate an immune response to the pathogen.  
CC Peptides are recognised by numerous T-helper cell clones within  
CC the context of a wide range of alleles of the human MHC.  
CC The peptides may be used in an antimalarial vaccine inducing Ab.  
CC response to P.falciparum.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15

RESULT 2  
43506

AAW35506 standard; peptide; 15 AA.

AC AAW35506;

DT 22-APR-1998 (first entry)

DE Universal T-cell epitope peptide SEQ ID NO:8.

XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;  
KW scaffold; inhibition; metastasis; wound healing; solid phase.

XX Unidentified.

XX WO9738011-A1.

XX 16-OCT-1997.

XX 03-APR-1997; 97WO-DE00146.

XX 03-APR-1996; 96DK-0000398.

XX (PEPR-) PEPRSEARCH AS.

XX Heegaard PMH, Jakobsen PH;

XX WPI; 1997-512645/47.

XX Non-dendritic peptide carrier linked to a solid phase - useful as a  
diagnostic agent and as a scaffold for production of chemical  
derivatives

XX Example 20; Page 124; 262pp; English.

XX A non-dendritic peptide carrier (A) has been developed which is coupled  
PS through a linker to a solid phase, forming a complex of (A)-solid phase.  
PS Where (A) comprises 10-50 amino acids capable of forming a secondary  
CC structure in a benign buffer after liberation from the solid phase, and  
CC further the (A)-solid phase complex comprises an immunogenic substance  
CC and/or an immune mediator coupled on (A). The present sequence  
CC represents a peptide used in an example from the present invention. An  
CC (A)-solid phase complex can be used as a scaffold for the production of  
CC chemical derivatives, characterised by covalently attaching molecules at  
CC attachment points. Alternatively (A) is used as a scaffold-peptide for  
CC the incorporation into an Immunostimulating Complex (Iscom) resulting an  
CC (A)-Iscom complex which is used for the chemical coupling of antigenic  
CC substances in an aqueous solution by conjugation. (A) derivatised with  
CC one or more peptides having fibronectin-, laminin- or vitronectin-like  
CC binding activities can be used for the promotion of cell-attachment to  
CC plastic surfaces, in particular to inhibit tumour growth and metastasis,  
CC and for promotion of wound healing. Also a derivatised (A) can be used  
CC for the selection of specifically-binding aptamers or as a diagnostic

CC agent. Such diagnostic-(A) molecules could be used to detect molecules  
CC derived from or indicative of pregnancy or of a disease, such as an  
CC infectious, autoimmune or cancerous disease.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 18; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15

RESULT 3

AAW11505  
ID AAW11505 standard; Protein; 15 AA.

XX AAW11505;

XX 24-SEP-1997 (first entry)

XX Tetanus toxoid universal Th epitope TT830.

XX Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;  
KW fusion protein; chimera; tetanus toxoid; helper T cell epitope;  
KW antigen presentation; ds.

XX Clostridium tetani.

XX WO9640789-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09988.

XX 07-JUN-1995; 95US-0484172.

XX (MEDA-) MEDAREX INC.

XX Deo YM, Goldstein J, Graziano R, Somasundaram C;

XX WPI; 1997-052242/05.

XX N-PSDB; AAT58127.

XX Recombinant, multi-specific anti-Fc receptor antibody molecules  
PT also comprise an anti-target portion, used for the treatment of  
PT cancer, autoimmune disease and pathogenic infection

XX Example 7; Fig 24; 115pp; English.

XX Synthetic DNA coding for the wild-type universal Th epitope from  
CC tetanus toxoid, designated TT830, was fused to the 3'-end of DNA  
CC encoding heavy chain sequences from the humanised anti-Fc gamma RI  
CC monoclonal antibody H22. The resulting fusion protein was shown to  
CC be significantly more efficient in antigen presentation and T cell  
CC stimulation than the TT830 epitope alone. A similar fusion  
CC construct was prepared coding for a mutant, antagonistic form of the  
CC epitope (designated TT833S) fused to the anti-Fc gamma RI. The  
CC Fab22-TT833S is at least 100 times more effective than TT833S in  
CC inhibiting T cell activation.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 18; Length 15;  
Best Local Similarity 100.0%; Pred. NO. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

DB 1 QYIKANSKFIGITEL 15

RESULT 4  
AAW67033  
ID AAW67033 standard; peptide; 15 AA.  
XX AC AAW67033;  
XX DT 15-DEC-1998 (first entry)  
XX DE Tetanus toxin fragment (residues 830-844).  
XX KW Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate;  
XX KW dendrimeric poly-lysine; epitope; tumour.  
XX OS Clostridium tetani.  
XX PN WO9843677-A1.  
08-OCT-1998.  
PF 27-MAR-1998; 98WO-EP01922.  
XX PR 27-MAR-1997; 97US-0041726.  
XX (INSP ) INST PASTEUR.  
XX PA Bay S, Cantacuzene D, Leclerc C, Lo-man R;  
XX PI WPI; 1998-557071/47.  
XX Carbohydrate peptide conjugate used as vaccine - comprises carrier  
XX PT with dendrimeric poly-lysine enabling multiple epitopes to be  
XX PT covalently attached  
XX PS Disclosure; Page 13; 55pp; English.  
XX The invention relates to a new carbohydrate peptide conjugate, which  
XX comprises a carrier with a dendrimeric poly-lysine enabling multiple  
XX epitopes to be covalently attached to it. Also claimed are: (1) an  
XX antibody purified from biological fluid or cells of organisms  
XX administered with the carbohydrate peptide conjugate, and (2) a diagnosis  
XX kit comprising antigen-specific antibodies elicited by immunisation with  
XX the carbohydrate peptide conjugate. The peptide conjugate, antibody and  
XX diagnosis kit are used to provide pharmaceutical compositions and  
XX vaccines against tumours. These can be used to support an immune response  
XX against viral infections caused by hepatitis virus, HIV or cytomegalo  
XX virus. They can be used to enhance immune responses, especially B- and T-  
XX cell responses, of humans and animals against bacterial infections. The  
XX carbohydrate peptide conjugate stimulates the antibody and T-cell  
XX response without stimulating undesired immune responses. The composition  
XX is capable of increasing the survival of tumour bearing humans and  
XX animals. The present sequence corresponds to residues 830-844 of tetanus  
XX toxin. The synthetic peptide corresponding to this sequence may be used  
XX as an epitope in a carbohydrate peptide conjugate.

Sequence 15 AA;  
Query Match 100.0%; Score 74; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
|||||

RESULT 5  
AAW71321  
ID AAW71321 standard; peptide; 15 AA.  
XX AC AAW71321;  
XX DT 26-NOV-1998 (first entry)

XX Universal helper T-cell epitope P2 derived from tetanus toxin.  
XX DE Liver stage; Plasmodium; Navy Yoelii Liver Stage 3 antibody; NYLS3;  
XX KW hepatic and erythrocytic stage protein; PyHEP17; vaccine;  
XX KW malaria parasite; teanus toxin; P2; helper T-cell epitope.  
XX OS Synthetic.  
XX OS Clostridium tetani.  
XX PN US5814617-A.  
XX PD 29-SEP-1998.  
XX PF 07-OCT-1994; 94US-0319704.  
XX PR 07-OCT-1994; 94US-0319704.  
XX PA (USNA ) US SEC OF NAVY.  
XX PI Charoenvit Y, Doolan DL, Hedstrom RC, Hoffman SL;  
XX DR WPI; 1998-541794/46.  
XX Vaccine for protecting mammal against infection by malaria caused by  
XX PT Plasmodium species - comprises a first nucleic acid encoding a first  
XX PT polypeptide capable of eliciting an immune reaction against an  
XX PT antigen expressed during the liver  
XX PS Disclosure; Column 12; 24pp; English.  
XX AAW71321-22 represent universal helper T-cell epitopes derived from  
XX tetanus toxin. They are used to enhance host immune response to  
XX vaccines. The specification describes a Plasmodium yoelii liver stage  
XX 17 kDa hepatic and erythrocytic stage protein designated PyHEP17. This  
XX protein elicits a response from an Igl monoclonal antibody designated  
XX Navy Yoelii Liver Stage 3 (NYLS3). This antibody does not recognise  
XX sporozoites, but does recognise P. yoelii liver stage parasites. NYLS3  
XX eliminates upto 90% of liver stage parasites. The specification  
XX describes a vaccine for reducing the severity or incidence of infection  
XX by a malaria parasite of the genus Plasmodium. The DNA vaccine comprises  
XX exon 1 and part of exon 2 of the PyHEP17 gene.

Sequence 15 AA;  
Query Match 100.0%; Score 74; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
|||||

RESULT 6  
AAW04051  
ID AAW04051 standard; peptide; 15 AA.  
XX AC AAW04051;  
XX DT 04-JAN-2000 (first entry)  
XX T-Helper epitope from tetanus toxoid.  
XX Covalently reactive antigen analog; CRAA; catalytic antibody;  
XX KW electrophilic reaction centre; phosphonate; boronate; vaccine;  
XX KW transition state analog; TSA; isostere; gp120; HIV-1; T-helper;  
XX KW tetanus; toxoid; B-T-epitope.  
XX OS Clostridium tetani.  
XX PN WO9948925-A1.  
XX

PD 30-SEP-1999.  
 XX  
 PF 23-MAR-1999; 99WO-US06325.  
 XX  
 PR 23-MAR-1998; 98US-0046373.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Paul S. Gololobov G. Smith L;  
 XX WPI; 1999-591076/50.  
 DR  
 XX  
 XX New covalently reactive antigen analogs used for treating e.g.  
 PT autoimmune diseases, lymphoproliferative disorders, cancers, microbial  
 PT infections, ischemic and reperfusion injury or septic shock -  
 XX  
 PS Disclosure; Page 86; 158pp; English.  
 XX  
 CC The patent discloses new covalently reactive antigen analogs (CRAA)  
 CC of formula X1-Y-E-X2, in which X1 and X2 represent peptide sequences  
 CC of an epitope of a disease-associated protein, Y is a positively  
 CC charged amino acid residue, preferably Lys or Arg, and E is an  
 CC electrophilic reaction centre, preferably a phosphonate or boronate  
 CC moiety. Depending on the identity of the epitope, the CRAA may be used  
 CC to stimulate production of catalytic antibodies specific for  
 CC predetermined antigens associated with particular medical disorders.  
 CC They may also be used to permanently inactivate endogenously produced  
 CC catalytic antibodies produced in certain autoimmune diseases as well as  
 CC in certain lymphoproliferative disorders.  
 CC Amongst the specifically exemplified CRAAs is one based on residues  
 CC 421-436 of a B-cell epitope of gp120 (see AAY04046) which may be used  
 CC to counter HIV-1 infections. When used as an immunogen, preferably this  
 CC CRAA is conjugated at its N-terminal to a T-helper epitope from tetanus  
 CC toxoid. The present sequence represents the T-helper epitope and  
 CC corresponds to residues 830-844 of the toxoid.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 74; DB 20; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QYIKANSKFIGITEL 15  
 Db | | | | | | | | | | | | | | |  
 1 QYIKANSKFIGITEL 15  
 RESULT 8  
 AAW73220  
 ID AAW73220 standard; Protein; 15 AA.  
 AC AAW73220;  
 XX  
 XX 25-JAN-1999 (first entry)  
 DT  
 XX  
 DE Tetanus toxoid epitope.  
 XX  
 KW Multispecific single chain antibody; antibody H22; tumour cell; therapy;  
 KW antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;  
 XX epidermal growth factor receptor; breast cancer; ovarian cancer.  
 OS Synthetic.  
 XX  
 PN US5837243-A.  
 XX  
 PD 17-NOV-1998.  
 XX  
 XX 07-JUN-1996; 96US-0661052.  
 PF  
 XX 07-JUN-1996; 96US-0661052.  
 PR  
 PR 07-JUN-1995; 95US-0484172.  
 XX  
 PA (MEDA-) MEDAREX INC.  
 XX  
 XX Deo YM, Goldstein J, Graziano R, Somasundaram C;  
 PI  
 XX WPI; 1999-023374/02.  
 DR  
 XX  
 PT Specific killing of tumour cells - using a multi-specific molecule  
 PT comprising an anti-Fc receptor antibody and a portion which binds to  
 PT a target cell  
 XX  
 PS Example 7; Column 27; 57pp; English.  
 XX  
 CC This sequence represents a tetanus toxoid epitope and is recognised  
 CC by the multispecific single chain antibody designated H22. The  
 CC antibody can be used in the method of the invention for inducing  
 CC antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell  
 CC which is characterised by overexpression of HER 2/neu or epidermal growth  
 CC factor receptor (EGFR), comprises contacting the tumour cell with a  
 CC multispecific protein molecule (preferably a single chain antibody)  
 CC comprising: (a) an anti-Fc receptor antibody or an antigen binding  
 CC fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which  
 CC binds to EGFR. The method can be used for treating cancers especially

30-SEP-1999.  
 XX  
 PF 23-MAR-1999; 99WO-US06325.  
 XX  
 PR 23-MAR-1998; 98US-0046373.  
 XX  
 PA (UYNE-) UNIV NEBRASKA.  
 XX  
 PI Paul S. Gololobov G. Smith L;  
 XX WPI; 1999-591076/50.  
 DR  
 XX  
 XX New covalently reactive antigen analogs used for treating e.g.  
 PT autoimmune diseases, lymphoproliferative disorders, cancers, microbial  
 PT infections, ischemic and reperfusion injury or septic shock -  
 XX  
 PS Disclosure; Page 86; 158pp; English.  
 XX  
 CC The patent discloses new covalently reactive antigen analogs (CRAA)  
 CC of formula X1-Y-E-X2, in which X1 and X2 represent peptide sequences  
 CC of an epitope of a disease-associated protein, Y is a positively  
 CC charged amino acid residue, preferably Lys or Arg, and E is an  
 CC electrophilic reaction centre, preferably a phosphonate or boronate  
 CC moiety. Depending on the identity of the epitope, the CRAA may be used  
 CC to stimulate production of catalytic antibodies specific for  
 CC predetermined antigens associated with particular medical disorders.  
 CC They may also be used to permanently inactivate endogenously produced  
 CC catalytic antibodies produced in certain autoimmune diseases as well as  
 CC in certain lymphoproliferative disorders.  
 CC Amongst the specifically exemplified CRAAs is one based on residues  
 CC 421-436 of a B-cell epitope of gp120 (see AAY04046) which may be used  
 CC to counter HIV-1 infections. When used as an immunogen, preferably this  
 CC CRAA is conjugated at its N-terminal to a T-helper epitope from tetanus  
 CC toxoid. The present sequence represents the T-helper epitope and  
 CC corresponds to residues 830-844 of the toxoid.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 74; DB 20; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QYIKANSKFIGITEL 15  
 Db | | | | | | | | | | | | | | |  
 1 QYIKANSKFIGITEL 15  
 RESULT 7  
 AAW67578  
 ID AAW67578 standard; peptide; 15 AA.  
 AC AAW67578;  
 XX  
 XX 02-MAR-1999 (first entry)  
 DT  
 XX  
 DE T-cell epitope peptide #4 for chimeric fimbrin/T-cell epitope peptide.  
 XX  
 KW Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;  
 KW immunogenic composition; immune response.  
 XX  
 OS Synthetic.  
 XX  
 PN US5843464-A.  
 XX  
 PD 01-DEC-1998.  
 XX  
 XX 02-JUN-1995; 95US-0460502.  
 PF  
 XX 02-JUN-1995; 95US-0460502.  
 PR  
 PA (OHIS ) UNIV OHIO STATE.  
 XX  
 XX Bakaletz LO, Kaumaya PTP;

CC breast cancer or ovarian cancer. The multispecific antibody can also  
CC be administered prophylactically to vaccinate a subject against infection  
CC by a target cell.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 20; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15

RESULT 9  
AAB45511  
AAB45511 standard; Protein; 15 AA.

AAB45511;

DT 26-FEB-2001 (first entry)

DE Tetanus P2 epitope SEQ ID NO: 23.

KW Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection;  
KW cancer; eosinophilia; vaccine; allergic rhinitis.

OS Clostridium tetani.

PN WO200065058-A1.

PD 02-NOV-2000.

PF 19-APR-2000; 2000WO-DK00205.

PR 23-APR-1999; 99DK-0000552.

PR 06-MAY-1999; 99US-0132811.

XX (MEBI-) M & E BIOTECH AS.

PA Klysner S;

DR WPI; 2000-672791/65.

XX Down-regulating interleukin 5 (IL-5) activity in humans by  
XX administering IL-5 and/or an IL-5 analogue, useful in the treatment,  
XX prophylaxis or amelioration of asthma or other chronic allergic  
XX conditions -

PS Example 1; Page 137; 172pp; English.

XX The present invention is concerned with methods of treating asthma,  
XX eosinophilia, allergic rhinitis and other allergic diseases. These  
XX involve the use of interleukin-5 (IL-5) analogues and modified IL-5  
XX proteins and their coding sequences to down-regulate IL-5 activity and  
XX thus reduce eosinophil numbers. The allergic diseases may be treated  
XX using autovaccines, nucleic acid vaccines or live vaccines. In addition,  
XX it is possible that they may be used in the treatment of cancer and  
XX helminthic infections.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15

RESULT 10

AAV82637

ID AAV82637 standard; peptide; 15 AA.

XX AC AAV82637;

XX DT 07-AUG-2000 (first entry)

DE Tetanus toxoid T cell epitope peptide SEQ ID NO:13.

KW T cell epitope; B cell epitope; allergy; allergen; antigenic;  
KW anti-allergic; antiasthmatic; antiinflammatory; dermatological;  
KW immunosuppressive; vaccine; rhinitis; sinusitis; bronchial asthma;  
KW atopic dermatitis; acute urticaria; chronic urticaria;  
KW gastro-intestinal syndrome; food allergen; oro-pharyngeal syndrome;  
KW anaphylactic reaction; drug hypersensitivity; allergic reaction.

XX Clostridium tetani.

OS Synthetic.

XX WO200006694-A2.

PD 10-FEB-2000.

PF 20-JUL-1999; 99WO-BE00092.

PR 30-JUL-1998; 98EP-0870167.

XX (UNIO ) UCB SA.

PI Saint-Remy J, Jacquemin M;

DR WPI; 2000-422470/36.

XX New compound for prevention and treatment of allergies comprises at  
XX least one allergen antigenic determinant recognized by a B cell and at  
XX least one antigenic determinant which does not trigger T cell  
XX activation -

XX Example 6; Page 30; 50pp; English.

XX The present invention describes a compound (I) for the prevention and/or  
XX treatment of allergy. The compound comprises at least one allergen  
XX antigenic determinant (i) recognised by a B cell or an antibody secreted  
XX by a B cell of a non-atopic individual and at least one antigenic  
XX determinant (ii) different from the allergen that triggers T cell  
XX activation. (I) has antiallergic, antiasthmatic, antiinflammatory,  
XX dermatological and immunosuppressive activities, and can be used in a  
XX vaccine. (I) may be used in a pharmaceutical or cosmetic medicament to  
XX treat and/or prevent allergies or a disease of allergic origin,  
XX especially hypersensitivities. These include rhinitis, sinusitis,  
XX bronchial asthma, atopic dermatitis, some forms of acute and chronic  
XX urticaria, gastro-intestinal syndromes associated with the ingestion of  
XX food allergens, oro-pharyngeal syndrome, anaphylactic reactions  
XX associated with drug hypersensitivities and/or a mixture of these. The  
XX use of (I) in the treatment of allergic conditions avoids the need for  
XX drug treatment, which often causes undesirable side-effects. Also, prior  
XX art drug therapies alleviate symptoms, but do not influence their  
XX causes, however (I) actually combats the cause of an allergic reaction.  
XX The present sequence represents a peptide, which is used in an  
XX example from the present invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15

RESULT 11



|          |           |   |
|----------|-----------|---|
|          | AAAY92625 | standard; Protein: 15 AA.   |
| XX       | AC AC     |   |
| XX       | XX XX     |   |
| DT       | OT DT     | 10-AUG-2000 (first entry)   |
| XX       | XX XX     | Foreign epitope P2.   |
| XX       | XX XX     | Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2;       |
| XX       | KW KW     | Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination;             |
| XX       | KW KW     | Cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer;     |
| XX       | KW KW     | prostate cancer; cell-associated peptide antigen.                         |
| XX       | XX XX     | Clostridium tetani.   |
| XX       | XX XX     | WO200020027-A2.   |
| PD       | PPD PD    | 13-APR-2000.  |
| PFPF     | PFPF PF   | 05-OCT-1999; 99WO-DK00525.  |
|          |           | 05-OCT-1998; 98DK-0001261.  |
|          |           | 20-OCT-1998; 98US-0105011.  |
|          | rd rd     | (MEBI-) M & E BIOTECH AS.   |
| XX       | XX XX     | Steina L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;           |
| XX       | PA PA     | Gautam A, Birk P, Karlsson G;   |
| PPI      | PPI PPI   | WPI: 2000-349917/30.  |
| DR       | DR DR     | N-PSDB; AAA09460.   |
| XX       | XX XX     | Inducing immune responses to weakly immunogenic, tumor associated         |
| PPT      | PPT PPT   | peptide antigens for the treatment of breast and prostate cancer          |
| XX       | XX XX     | Example 1; Page 213; 22Opp; English.                                      |
| PS       | PS PS     | The claims detail a method for inducing immune responses against weakly   |
| CC       | CC CC     | immunogenic cell-associated peptide antigens (PA) such as those           |
| CC       | CC CC     | associated with cancers (i.e. self-proteins), for example, human          |
| CC       | CC CC     | prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or       |
| CC       | CC CC     | fibroblast growth factor 8b (FGF8b). The method comprises effecting       |
| CC       | CC CC     | simultaneous presentation by antigen producing cells (APCs) of the        |
| CC       | CC CC     | animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)     |
| CC       | CC CC     | group derived from the PA and/or at least 1 B-cell group derived from the |
| CC       | CC CC     | cell-associated PA; and (2) at least 1 first T helper cell group which is |
| CC       | CC CC     | foreign to the animal. Analogues of human PSM, human Her2 and             |
| CC       | CC CC     | human/murine FGF8b comprising a substantial part of all known and         |
| CC       | CC CC     | predicted CTL and B-cell epitopes of the respective PA and including at   |
| CC       | CC CC     | least one foreign T helper epitope (e.g. P2 and/or P30) are also claimed. |
| CC       | CC CC     | The method is used to treat prostate, prostate/breast or breast cancer    |
| CC       | CC CC     | when the PA is human PSM, FGF8b and Her2, respectively.                   |
| SQ       | XX SQ     | Sequence 15 AA;   |
|          |           | Query Match 100.0%; Score 74; DB 21; Length 15;                           |
|          |           | Best Local Similarity 100.0%; Pred. No. 3.3e-07;                          |
|          |           | Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;               |
| OY       | OY OY     | 1 QYIKANSKFIGITEL 15  |
|          |           |   |
| Db       | Db Db     | 1 QYIKANSKFIGITEL 15  |
|          |           | RESULT 12   |
| AAI84427 | AAI84427  | ID AAI84427 standard; Peptide: 15 AA.                                     |
| XX       | XX XX     | AAY84427;   |
| XX       | XX XX     | 25-JUL-2000 (first entry)   |
| DF       | DF DF     |   |
| XX       | XX XX     |   |

KW EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen;  
 KW Pfg27; antiparasitic; prevention; anti-CDC/NIIHALVAC-1 antibody.

XX Clostridium tetani.

PN WO200011179-A1.

XX 02-MAR-2000.

PF 19-AUG-1999; 99WO-US18869.

XX 21-AUG-1998; 98US-0097703.

XX (NATM-) NAT INST IMMUNOLOGY.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Lal AA, Shi YP, Hasnain SE;

PI WPI; 2000-237654/20.

PT Novel recombinant protein as vaccine for treating malarial infection  
 PT comprises antigenic peptides obtained from different stages of  
 PT plasmodium falciparum life cycle

PS Claim 2; Page 17; 52pp; English.

XX The present sequence is the tetanus toxoid P589, derived  
 CC from Clostridium tetani. It is used in the construction of recombinant  
 CC protein CDC/NIIHALVAC-1, which is a multivalent, multistage malarial  
 CC vaccine. The recombinant protein comprises, melittin signal peptide,  
 CC (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes  
 CC from circumsporozoite protein (CSP), sporozoite surface protein-2  
 CC (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1  
 CC (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding  
 CC antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete  
 CC specific antigen, Pfg27. These epitopes were obtained at different stages  
 CC of the life cycle of P. falciparum. CDC/NIIHALVAC-1 vaccine has  
 CC antiparasitic activity and can be used for treatment and prevention of  
 CC malarial infections. Anti-CDC/NIIHALVAC-1 antibodies can be used for  
 CC detecting P. falciparum in biological samples.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07; Mismatches 0; Gaps 0;  
 Matches 15; Conservative 0;

DB 1 QYIKANSKFIGITEL 15  
 |||||  
 1 QYIKANSKFIGITEL 15

RESULT 14

AA44763

ID AAY44763 standard; peptide; 15 AA.

XX AAY44763;

XX 04-MAY-2000 (first entry)

XX Tetanus toxoid protein derived T-cell activating epitope P2.

XX Surface layer protein; S-layer secretion signal; antibiotic; vaccine;  
 KW recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff;  
 KW antibacterial enzyme; surface glycoprotein; T-cell activating epitope;  
 KW P2; tetanus toxoid; IPNV; Infectious pancreatic necrosis virus.

XX Clostridium tetani.

XX WO200004170-A1.

XX 27-JAN-2000.

PF 14-JUL-1999; 99WO-CA00637.

XX 14-JUL-1998; 98CA-2237704.

XX (UYBR-) UNIV BRITISH COLUMBIA.

XX Smit J;

PI WPI; 2000-182434/16.

XX Cleavage of Caulobacter produced recombinant fusion proteins useful for  
 XX producing vaccine peptides

XX Example 2; Page 16; 33pp; English.

XX The patent discloses a method for cleaving a recombinant fusion protein  
 CC which is produced by Caulobacter and consists of Caulobacter surface  
 CC layer (S-layer) protein (containing the C-terminal secretion signal) and  
 CC a target protein heterologous to Caulobacter. The cleavage of target  
 CC protein from the S-layer protein is carried out under mild acid  
 CC conditions so that cleavage occurs at aspartate-proline dipeptide site  
 CC without solubilising the protein. The cleavage is accomplished while the  
 CC fusion protein is in an insoluble aggregate form which facilitates  
 CC purification of the protein. The method is useful for producing pure  
 CC proteins including recombinant human and animal therapeutic antibiotic  
 CC and vaccine peptides, enzymes, protein polymers, and antibacterial  
 CC enzymes for foodstuffs.

XX The present sequence is a T-cell activating epitope P2 derived  
 CC from tetanus toxoid protein. This sequence was fused to a DNA encoding  
 CC a fragment of infectious pancreatic necrosis virus surface glycoprotein  
 CC which is a vaccine candidate. This chimeric protein was in turn fused to  
 CC DNA encoding C. crescentus S-layer secretion signal (corresponds to the  
 CC C-terminal portion of the S-layer protein from amino acid 690 onwards and  
 CC contains native Asp-Pro site) for construction of a recombinant  
 CC fusion construct which is expressed in Caulobacter and then cleaved  
 CC to recover the vaccine candidate protein.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 21; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

DB 1 QYIKANSKFIGITEL 15

RESULT 15

AAE11763

ID AAE11763 standard; peptide; 15 AA.

XX AAE11763;

XX 18-DEC-2001 (first entry)

XX Clostridium tetani P2 epitope.

XX Amyloid protein; neuroprotective; nootropic; immunostimulant; vaccine;  
 KW Alzheimer's disease; anticonvulsant; gene therapy; Pick's disease;  
 KW antidiabetic; systemic amyloidosis; maturity onset diabetes; ALS;  
 KW amyotrophic lateral sclerosis; Parkinson's disease; encephalopathy;  
 KW Huntington's disease; fronto-temporal dementia; P2 epitope.

XX Clostridium tetani.

XX WO200162284-A2.

XX 30-AUG-2001.

XX 19-FEB-2001; 2001WO-DK00113.

XX 21-FEB-2000; 2000DK-0000265.

```

PR 01-NAR-2000; 2000US-186295P.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Birk P, Jensen MR, Nielsen KG;
XX
XX WPI; 2001-589796/66.
XX N-PSDB; AAD18755.
XX
XX In vivo down-regulation of amyloid protein for the treatment of
PT Alzheimer's, comprises presenting an amyloidogenic polypeptide or its
PT subsequence and/or at least one analogue of the amyloidogenic
PT polypeptide to the immune system
XX
XX Example 3; Page 117; 120pp; English.
XX
XX The invention relates to a method for in vivo down-regulation of amyloid
CC protein such as beta amyloid (Abeta) in an animal, including human. The
CC method comprising presenting to the animal's immune system an
CC immunogenically effective amount of at least one amyloidogenic protein
CC or its subsequence and/or at least one analogue of the amyloidogenic
CC polypeptide. The amyloidogenic protein or its subsequence, and its
CC analogue is useful for the preparation of an immunogenic composition
CC comprising an adjuvant for down-regulating amyloid in an animal. They are
CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's
CC disease or other diseases characterised by amyloid deposits. They are
CC also useful in the treatment of systemic amyloidosis, maturity onset
CC diabetes, Parkinson's disease, Huntington's disease, fronto-temporal
CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and
CC prion-related transmissible spongiform encephalopathies. They are also
CC useful for inducing production of antibodies against an amyloidogenic
CC polypeptide. The present sequence is Clostridium tetani P2 epitope
XX related to the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 100.0%; Score 74; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 OYIKANSKFIGITEL 15
DB 1 OYIKANSKFIGITEL 15

```

Search completed: October 10, 2002, 16:00:56  
Job time : 5.02108 secs

GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 1.76205 Seconds  
(without alignments)  
329.613 Million cell updates/sec

Title: US-09-787-126-34

Perfect score: 74

Sequence: 1 QV1KANSRFIGITEL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 74    | 100.0       | 1314   | 1 TETX_CLOTE | P04958 clostridium  |
| 2          | 44    | 59.5        | 66     | 1 VGB4_BPM15 | Q05301 mycobacteri  |
| 3          | 42.5  | 57.4        | 1682   | 1 MSP1_PLAF3 | P19598 plasmodium   |
| 4          | 42.5  | 57.4        | 1701   | 1 MSP1_PLAF5 | P13819 plasmodium   |
| 5          | 42.5  | 57.4        | 1701   | 1 MSP1_PLAFM | P08569 plasmodium   |
| 6          | 42.5  | 57.4        | 1726   | 1 MSP1_PLAF6 | P04934 plasmodium   |
| 7          | 42.5  | 57.4        | 1726   | 1 MSP1_PLAF7 | P04935 plasmodium   |
| 8          | 41    | 55.4        | 204    | 1 PYRC_SERMA | Q9s3s1 serratia ma  |
| 9          | 41    | 55.4        | 899    | 1 V120_HSVSA | Q01055 herpesvirus  |
| 10         | 40    | 54.1        | 194    | 1 ACPD_HAEIN | P43013 haemophilus  |
| 11         | 40    | 54.1        | 601    | 1 PEF1_LACLC | P54124 lactococcus  |
| 12         | 40    | 54.1        | 601    | 1 PEPF_LACLA | Q9cev7 lactococcus  |
| 13         | 40    | 54.1        | 644    | 1 YHJ9_YEAST | P38694 saccharomyc  |
| 14         | 39    | 52.7        | 213    | 1 RAD_MYCCA  | P10251 mycoplasma   |
| 15         | 38    | 51.4        | 256    | 1 YD83_METJA | Q58778 methanococc  |
| 16         | 38    | 51.4        | 287    | 1 TRUB_AQUAE | Q66922 aquifex aeo  |
| 17         | 38    | 51.4        | 572    | 1 HEMA_P13HT | P12562 human parai  |
| 18         | 37    | 50.0        | 191    | 1 Y096_HAEIN | P43940 haemophilus  |
| 19         | 37    | 50.0        | 445    | 1 GNT1_HUMAN | P26572 homo sapien  |
| 20         | 37    | 50.0        | 447    | 1 GNT1_MOUSE | P27808 mus musculu  |
| 21         | 37    | 50.0        | 447    | 1 GNT1_RABIT | P27115 oryctolagus  |
| 22         | 37    | 50.0        | 447    | 1 GNT1_RAT   | Q09325 rattus norv  |
| 23         | 37    | 50.0        | 490    | 1 Y032_BORBU | O51063 borrelia bu  |
| 24         | 37    | 50.0        | 510    | 1 G6PD_ASPNG | P48826 aspergillus  |
| 25         | 37    | 50.0        | 511    | 1 G6PD_EMENI | P41764 emericella   |
| 26         | 37    | 50.0        | 548    | 1 YDD2_SCHPO | O10428 schizosacch  |
| 27         | 36    | 48.6        | 169    | 1 Y358_BUCAI | P57439 buchnera ap  |
| 28         | 36    | 48.6        | 258    | 1 MIP_CHLPN  | Q9z7p3 chlamydia p  |
| 29         | 36    | 48.6        | 296    | 1 YD01_CLOAB | P33659 clostridium  |
| 30         | 36    | 48.6        | 333    | 1 DPOB_XENLA | O57383 xenopus lae  |
| 31         | 36    | 48.6        | 451    | 1 MORD_BACSU | Q03522 bacillus su  |
| 32         | 36    | 48.6        | 461    | 1 NIFN_RHOCA | P19077 rhodobacter  |
| 33         | 36    | 48.6        | 495    | 1 G6PD_PICJA | P11410 picchia jadi |

|    |    |      |      |              |                    |
|----|----|------|------|--------------|--------------------|
| 34 | 36 | 48.6 | 530  | 1 YND1_YEAST | P40009 saccharomyc |
| 35 | 36 | 48.6 | 774  | 1 RRP3_INCBE | P21770 influenza c |
| 36 | 36 | 48.6 | 774  | 1 RRP3_INCBJ | P13877 influenza c |
| 37 | 36 | 48.6 | 1630 | 1 MSP1_PLAFK | P04932 plasmodium  |
| 38 | 36 | 48.6 | 1639 | 1 MSP1_PLAFW | P04933 plasmodium  |
| 39 | 35 | 47.3 | 176  | 1 NUGC_SPIOL | Q9m318 spinacia ol |
| 40 | 35 | 47.3 | 261  | 1 CABV_CHICK | P04354 gallus gall |
| 41 | 35 | 47.3 | 294  | 1 CDD_ECOLI  | P13652 escherichia |
| 42 | 35 | 47.3 | 321  | 1 YDG7_SCHPO | O10494 schizosacch |
| 43 | 35 | 47.3 | 329  | 1 DHOA_EMENI | P25415 emericella  |
| 44 | 35 | 47.3 | 353  | 1 4IKD_LACHE | P17212 lactobacill |
| 45 | 35 | 47.3 | 402  | 1 VGLD_HVEA  | P24872 equine herp |

## ALIGNMENTS

RESULT 1  
TETX\_CLOTE  
ID TETX\_CLOTE STANDARD; PRT; 1314 AA.  
AC P04958;  
DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Tetanus toxin precursor (EC 3.4.24.68) (Pentoxylisin).  
OS Clostridium tetani.  
OG Plasmid.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87053814; PubMed=3536478;  
RA Elsel U., Jarausch W., Goretzki K., Henschen A., Engels J.,  
RA Weller U., Hudel M., Habermann E., Niemann H.:  
RT "Tetanus toxin: Primary structure, expression in E. coli, and  
RT homology with botulinum toxins.";  
RL EMBO J. 5:2495-2502(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CN3911;  
RA Fairweather N.F., Lyness V.A.;  
RT "The complete nucleotide sequence of tetanus toxin.";  
RL Nucleic Acids Res. 14:7809-7812(1986).  
RN [3]  
RP SEQUENCE OF 742-1314 FROM N.A.  
RX MEDLINE=86085672; PubMed=3510187;  
RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;  
RT "Cloning, nucleotide sequencing, and expression of tetanus toxin  
RT fragment C in Escherichia coli.";  
RL J. Bacteriol. 165:21-27(1986).  
RN [4]  
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.  
RX MEDLINE=90201034; PubMed=2108021;  
RA Krieglstein K., Henschen A., Weller U., Habermann E.;  
RT "Arrangement of disulfide bridges and positions of sulfhydryl groups  
RT in tetanus toxin.";  
RL Eur. J. Biochem. 188:39-45(1990).  
RN [5]  
RP PARTIAL SEQUENCE.  
RX MEDLINE=92037649; PubMed=1935979;  
RA Krieglstein K.G., Henschen A.H., Weller U., Habermann E.;  
RT "Limited proteolysis of tetanus toxin. Relation to activity and  
RT identification of cleavage sites.";  
RL Eur. J. Biochem. 202:41-51(1991).  
RN [6]  
RP IDENTIFICATION AS ZINC-PROTEASE.  
RX MEDLINE=93010948; PubMed=1396558;  
RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,  
RA Montecucco C.;  
RT "Tetanus toxin is a zinc protein and its inhibition of  
RT neurotransmitter release and protease activity depend on zinc.";

EMBO J. 11:3577-3583(1992).  
[7]  
RN IDENTIFICATION OF SUBSTRATE.  
RP MEDLINE-93063293; PubMed-1331807;  
RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,  
RT Dasgupta B.R., Montecucco C.;  
"Tetanus and botulinum-B neurotoxins block neurotransmitter release  
by proteolytic cleavage of synaptobrevin.";  
RL Nature 359:832-835(1992).  
[8]  
RN X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.  
RX MEDLINE-97475217; PubMed-9334741;  
RA Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,  
Sax M.;  
"Structure of the receptor binding fragment HC of tetanus  
neurotoxin.";  
RL Nat. Struct. Biol. 4:788-792(1997).  
CC -!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER  
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED  
AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD  
WHERE IT CAN MOVE THROUGH POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT  
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC  
ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-1-PHE-77  
BOND OF SYNAPTOSOMAL VESICLES.  
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-1-PHE-77 BOND IN  
SYNAPTOSOMAL VESICLES.  
CC -!- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO  
YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE  
AND ARE NON-TOXIC AFTER SEPARATION.  
CC -!- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO  
GANGLIOSIDE RECEPTORS.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27.  
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CC  
CC EMBL; X04436; CAA28033.1; -  
DR EMBL; M12739; AAA23282.1; -  
DR EMBL; X06214; CAA29564.1; -  
DR PIR; A25689; BTCLTN.  
DR PDB; 1AF9; 29-APR-98.  
DR PDB; 1A8D; 14-OCT-98.  
DR MEROPS; M27.001; -  
DR InterPro; IPR000395; Bontoxilysin.  
DR InterPro; IPR000130; Zn\_Mtpeptidse.  
DR Pfam; PF01742; Peptidase\_M27; 1.  
DR PRINTS; PR00760; BONTOXILYSIN.  
DR ProDom; PD001963; Bontoxilysin; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;  
KW 3D-structure.  
FT INIT MET 0 0  
FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.  
FT CHAIN 457 1314 TETANUS TOXIN HEAVY CHAIN.  
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 233 233 BY SIMILARITY.  
FT METAL 236 236 ZINC (CATALYTIC) (BY SIMILARITY).  
FT TRANSMEM 226 246 POTENTIAL.  
FT TRANSMEM 669 689 POTENTIAL.  
FT DISULFID 438 466 INTERCHAIN.  
FT DISULFID 1076 1092  
SQ SEQUENCE 1314 AA; 150550 MW; 134C3657133EF8D CRC64;  
Query Match 100.0%; Score 74; DB 1; Length 1314;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15

DB 829 QYIKANSKFIGITEL 843  
RESULT 2  
VG84\_BPML5  
ID VG84\_BPML5 STANDARD; PRT; 66 AA.  
AC Q05301;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Gene 84 protein (GP84).  
GN 84.  
OS Mycobacteriophage L5.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=31757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-93211289; PubMed-8459766;  
RA Hatfull G.F., Sarkis G.J.;  
"DNA sequence, structure and gene expression of mycobacteriophage L5:  
a phage system for mycobacterial genetics.";  
RT Mol. Microbiol. 7:395-405(1993).  
CC  
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CC  
CC EMBL; Z18946; CAA79460.1; -  
DR PIR; S31029; S31029.  
SQ SEQUENCE 66 AA; 7424 MW; 9C7104C7A4FA74A5 CRC64;  
Query Match 59.5%; Score 44; DB 1; Length 66;  
Best Local Similarity 57.1%; Pred. No. 0.21;  
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 2 YIKANSKFIGITEL 15  
DB 50 YIKRNGKFGVTWEV 63  
RESULT 3  
MSP1\_PLAF3  
ID MSP1\_PLAF3 STANDARD; PRT; 1682 AA.  
AC P19598; Q25921;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)  
DE (PMSA) (P190).  
GN MSP-1.  
OS Plasmodium falciparum (Isolate ro-33 / Ghana).  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5834;  
RN [1]  
RP SEQUENCE OF 1-1061 FROM N.A.  
RX MEDLINE-88166657; PubMed-3327688;  
RA Certa U., Rotmann D., Matile H., Reber-Liske R.;  
"A naturally occurring gene encoding the major surface antigen  
precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";  
RL EMBO J. 6:4137-4142(1987).  
RN [2]  
RP SEQUENCE OF 1032-1682 FROM N.A.  
RX MEDLINE-95354793; PubMed-7628566;  
RA Tolle R., Bujard H., Cooper J.A.;  
"Plasmodium falciparum: variations within the C-terminal region of  
merozoite surface antigen-1.";  
RL Exp. Parasitol. 81:47-54(1995).  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor



(Potential).

-1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.

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-----

EMBL; X05624; CAA29112.1; --  
PIR; A26868; A26868.  
PIR; B25120; B25120.  
InterPro; IPR000561; EGF-like.  
Pfam; PF00008; EGF; 1.  
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
Transmembrane; GPI-anchor.  
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
KW Transmembrane; GPI-anchor.  
FT SIGNAL 1 19 POTENTIAL.  
CHAIN 20 1701 MEROZOITE SURFACE PROTEIN 1.  
CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 239 239 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 470 470 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 536 536 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 607 607 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 802 802 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 899 899 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 919 919 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 965 965 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 991 991 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 1089 1089 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 1196 1196 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 1588 1588 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 1701 AA; 193768 MW; 3FC2EC59AF96EA98 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1701;  
Best Local Similarity 60.0%; Pred. No. 11;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 OYIKANSKFI-GITE 14  
I:::||||| |::|

Db 1001 QFVKSNSKVIITGLTE 1015

RESULT 6

MSPL\_PLAFC STANDARD; PRT; 1726 AA.  
AC P04934;  
13-AUG-1987 (Rel. 05, Created)  
01-MAR-1989 (Rel. 10, Last sequence update)  
01-OCT-1996 (Rel. 34, Last annotation update)  
DE Merozoite surface protein 1 precursor (Merozoite surface antigens) (PMSA) (P195).  
DE MSP-1.  
GN Plasmodium falciparum (isolate Camp / Malaysia).  
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5835;  
RN [1]  
RP SEQUENCE OF 1-1103 FROM N.A.  
RX MEDLINE=86205236; PubMed=3517809;  
RA Weber J.L., Leininger W.M., Lyon J.A.;  
RT "Variation in the gene encoding a major merozoite surface antigen of the human malaria parasite Plasmodium falciparum.";  
RT Nucleic Acids Res. 14:3311-3323(1986).  
RN [2]  
RP SEQUENCE OF 1104-1726 FROM N.A.  
RX MEDLINE=88143999; PubMed=3278296;  
RA Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;  
RT "Merozoite surface protein sequence from the Camp strain of the human malaria parasite Plasmodium falciparum.";  
RT Nucleic Acids Res. 16:1206-1206(1988).

-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (potential).

-1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.

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-----

EMBL; X03831; CAA27446.1; --  
PIR; A23386; SAZQGM.  
InterPro; IPR000561; EGF-like.  
Pfam; PF00008; EGF; 1.  
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
Transmembrane; GPI-anchor.  
KW Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;  
KW Transmembrane; GPI-anchor.  
FT SIGNAL 1 19 POTENTIAL.  
CHAIN 20 1726 MEROZOITE SURFACE PROTEIN 1.  
CARBOHYD 133 133 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 272 272 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 501 501 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 567 567 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 638 638 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 924 924 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 944 944 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 990 990 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 1016 1016 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 1114 1114 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 1221 1221 N-LINKED (GLCNAC. .) (POTENTIAL).  
CARBOHYD 1613 1613 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 1726 AA; 196197 MW; DD8AD45FA352BCF3 CRC64;

Query Match 57.4%; Score 42.5; DB 1; Length 1726;  
Best Local Similarity 60.0%; Pred. No. 12;  
Matches 9; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

OY 1 OYIKANSKFI-GITE 14  
I:::||||| |::|

Db 1026 QFVKSNSKVIITGLTE 1040

RESULT 7

MSPL\_PLAFC STANDARD; PRT; 1726 AA.  
AC P50495;  
01-OCT-1996 (Rel. 34, Created)  
01-OCT-1996 (Rel. 34, Last sequence update)  
01-OCT-1996 (Rel. 34, Last annotation update)  
DE Merozoite surface protein 1 precursor (Merozoite surface antigens) (PMSA) (P195).  
DE MSP-1.  
GN Plasmodium falciparum (isolate Palo Alto / Uganda).  
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=57270;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89005525; PubMed=3049134;  
RA Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,  
RA Siddiqui W.A.;  
RT "Plasmodium falciparum: gene structure and hydropathy profile of the major merozoite surface antigen (gp195) of the Uganda-Palo Alto isolate.";  
RT Exp. Parasitol. 67:1-11(1988).  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (potential).  
CC -1- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 kDa, 42 kDa AND 19 kDa ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.





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Db 124 QYTSNATFTGLSE 137
RESULT 10
ACPD_HAEIN STANDARD; PRT; 194 AA.
AC P43013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP
DE phosphodiesterase).
GN ACPD OR H11366.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=96186898; PubMed=8635745;
RX Chandler M.S., Smith R.A.;
"Characterization of the Haemophilus influenzae topA locus: DNA
topoisomerase I is required for genetic competence.";
RL Gene 169:25-31(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shrivley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: CONVERTS HOLO-ACP TO APO-ACP BY HYDROLYTIC CLEAVAGE OF
CC THE PHOSPHOPANTHEINE RESIDUE FROM ACP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: [Acyl-carrier protein] + H(2)O -> 4'.
CC phosphopantetheine + apoprotein.
CC -1- SIMILARITY: BELONGS TO THE ACPD FAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U20964; AAC43728.1; -
DR EMBL; U32816; AAC23013.1; -
DR TIGR; H11366; -
KW Hydrolase; Complete proteome.
SQ SEQUENCE 194 AA; 21208 MW; A8AEC9D00829522C CRC64;

Query Match 54.1%; Score 40; DB 1; Length 194;
Best Local Similarity 53.3%; Pred. No. 3.5;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QYKANSKFIGITEL 15
|||: |||||:
Db 147 QYKRSILGFIGITDV 161

RESULT 11
PEFL_LACLC STANDARD; PRT; 601 AA.
ID PEFL_LACLC

Db 124 QYTSNATFTGLSE 137
RESULT 10
ACPD_HAEIN STANDARD; PRT; 194 AA.
AC P43013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP
DE phosphodiesterase).
GN ACPD OR H11366.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=96186898; PubMed=8635745;
RX Chandler M.S., Smith R.A.;
"Characterization of the Haemophilus influenzae topA locus: DNA
topoisomerase I is required for genetic competence.";
RL Gene 169:25-31(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kierlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shrivley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: CONVERTS HOLO-ACP TO APO-ACP BY HYDROLYTIC CLEAVAGE OF
CC THE PHOSPHOPANTHEINE RESIDUE FROM ACP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: [Acyl-carrier protein] + H(2)O -> 4'.
CC phosphopantetheine + apoprotein.
CC -1- SIMILARITY: BELONGS TO THE ACPD FAMILY.
CC -----
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CC -----
DR EMBL; U20964; AAC43728.1; -
DR EMBL; U32816; AAC23013.1; -
DR TIGR; H11366; -
KW Hydrolase; Complete proteome.
SQ SEQUENCE 194 AA; 21208 MW; A8AEC9D00829522C CRC64;

Query Match 54.1%; Score 40; DB 1; Length 194;
Best Local Similarity 53.3%; Pred. No. 3.5;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QYKANSKFIGITEL 15
|||: |||||:
Db 147 QYKRSILGFIGITDV 161

RESULT 12
PEPF_LACLA STANDARD; PRT; 601 AA.
ID PEPF_LACLA
AC Q9CEV7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Oligoendopeptidase F homolog (EC 3.4.24.-).
GN PEPF OR L11727.

AC P54124; P94880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oligoendopeptidase F, plasmid (EC 3.4.24.-).
GN PEPF1 OR PEPF.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OG Plasmid pLP763.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=NCDO 763;
RX MEDLINE=95096044; PubMed=7798200;
RX Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.;
"Biochemical and genetic characterization of PEPF, an oligopeptidase
from Lactococcus lactis.";
RL J. Biol. Chem. 269:32070-32076(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=NCDO 763;
RX MEDLINE=97352670; PubMed=9209029;
RX Nardi M., Renault P., Monnet V.;
"Duplication of the pepf gene and shuffling of DNA fragments on the
lactose plasmid of Lactococcus lactis.";
RL J. Bacteriol. 179:4164-4171(1997).
CC -1- FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO
CC ACIDS WITH A RATHER WIDE SPECIFICITY.
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
CC -----
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CC -----
DR EMBL; Z32522; CAA83534.1; -
DR EMBL; X99796; CAA68133.1; -
DR MEROPS; M03.007; -
DR InterPro; IPR001567; Peptidase_M3.
DR Pfam; PF01432; Peptidase_M3; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
KW Hydrolase; Metalloprotease; Zinc; Plasmid.
FT METAL 387 387 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 388 388 BY SIMILARITY.
FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 394 394 ZINC (CATALYTIC) (BY SIMILARITY).
FT CONFLICT 518 518 F -> S (IN REF. 2).
SQ SEQUENCE 601 AA; 69674 MW; C8B5C519FFA2F787 CRC64;

Query Match 54.1%; Score 40; DB 1; Length 601;
Best Local Similarity 46.7%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYKANSKFIGITEL 15
|||: | :|||:|
Db 284 RYELRKKILGIDTL 298

RESULT 12
PEPF_LACLA STANDARD; PRT; 601 AA.
ID PEPF_LACLA
AC Q9CEV7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Oligoendopeptidase F homolog (EC 3.4.24.-).
GN PEPF OR L11727.

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VIII.":
Science 265:2077-2082(1994).
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
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-----
EMBL: U00062; AAB68915.1;
PIR: S46746; S46746
SGD: S0001081; YHR039C.
InterPro: IPR002086; Aldehyde_dehydr.
Pfam: PF001171; aldedh; 1.
PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; 1.
KW Hypothetical protein; Oxidoreductase.
ACT_SITE 354 354 BY SIMILARITY.
FT ACT_SITE 389 389 BY SIMILARITY.
SQ SEQUENCE 644 AA; 71320 MW; 54DADDAEB2A16D4D CRC64;
Query Match 54.1%; Score 40; DB 1; Length 644;
Best Local Similarity 60.08; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 QYIKANSKFIGITEL 15
DB 38 QIQDNQKLGITFL 52
I I I I I I I
I I I I I I I
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RESULT 14
KAD_MYCCA STANDARD; PRT; 213 AA.
ID KAD_MYCCA
AC P10251; 1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
DE ADK.
GN MYCOPLASMA CAPRICOLUM.
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Entomoplasmataceae.
OC NCBI_TaxID=2095;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC 27343 / KID:
RC MEDLINE=88142549; PubMed=3481422;
RA Ohkubo S., Muto A., Kawachi Y., Yamao F., Osawa S.;
RT "The ribosomal protein gene cluster of Mycoplasma capricolum.";
RT Mol. Gen. Genet. 210:314-322(1987).
CC -!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -!- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
-----
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-----
EMBL: X06414; CAA29724.1;
PIR: S02851; K1YMC.
HSSP: P27142; 121N.
InterPro: IPR000850; Adenylate_kin.
DR Pfam: PF00406; adenylatekinase; 1.

```

Job time : 4.76205 secs

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DR PRINTS; PR00094; ADENYLTKINASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; ATP-binding.
FT NP_BIND 7 15 ATP (BY SIMILARITY).
SQ SEQUENCE 213 AA; 24616 MW; FBCFA426B6F92E16 CRC64;

Query Match          52.7%; Score 39; DB 1; Length 213;
Best Local Similarity 72.7%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YIKANSKEFIGI 12
DB 183 YFKTNSKFEI 193

RESULT 15
YD83_METJA STANDARD; PRT; 256 AA.
AC Q58778;
DT 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1383 precursor.
GN MJ1383.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE-96337999; PubMed-8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: TO M.JANNASCHII MJ0761.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; U67578; AAB99393.1;
CC TIGR; MJ1383;
CC InterPro; IPR001130; TatD.
CC Pfam; PF01026; TatD_DNase; 1.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 256 HYPOTHETICAL PROTEIN MJ1383.
SQ SEQUENCE 256 AA; 29036 MW; 6D26F427EAB54675 CRC64;

Query Match          51.4%; Score 38; DB 1; Length 256;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YIKANSKEFIGITEL 15
DB 89 YINYSRVVGIGEI 102

Search completed: October 10, 2002, 16:04:53

```

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 10, 2002, 12:48:46 ; Search time 4.83434 Seconds  
(without alignments)  
536.769 Million cell updates/sec

Title: US-09-787-126-34  
Perfect score: 74  
Sequence: 1 QYIKANSKFIGITEL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description         |
|------------|-------|-------------|--------|-----------|---------------------|
| 1          | 74    | 100.0       | 1310   | 2 Q93N27  | Q93n27 clostridium  |
| 2          | 44.5  | 60.1        | 60     | 7 Q31585  | Q31585 salmo salar  |
| 3          | 44.5  | 60.1        | 71     | 7 Q9XRJ9  | Q9xrj9 salvelinus   |
| 4          | 44.5  | 60.1        | 85     | 7 Q95IS2  | Q95is2 salmo salar  |
| 5          | 44.5  | 60.1        | 85     | 7 Q95HY1  | Q95hy1 salmo salar  |
| 6          | 44.5  | 60.1        | 86     | 7 Q95HX4  | Q95hx4 salmo salar  |
| 7          | 44.5  | 60.1        | 244    | 7 Q31590  | Q31590 salmo salar  |
| 8          | 44    | 59.5        | 546    | 10 Q9XG37 | Q9xg37 guillardia   |
| 9          | 43.5  | 58.8        | 67     | 7 Q31578  | Q31578 salmo salar  |
| 10         | 43    | 58.1        | 180    | 16 Q9CF66 | Q9cf66 lactococcus  |
| 11         | 43    | 58.1        | 250    | 9 Q9MCL7  | Q9mcl7 streptococ   |
| 12         | 43    | 58.1        | 252    | 9 Q9XJIE8 | Q9xje8 lactococcus  |
| 13         | 43    | 58.1        | 302    | 11 Q9CRV4 | Q9crv4 mus musculus |
| 14         | 43    | 58.1        | 309    | 11 Q9CYD2 | Q9cyd2 mus musculus |
| 15         | 43    | 58.1        | 899    | 12 Q9YTK4 | Q9ytk4 ateline her  |
| 16         | 42.5  | 57.4        | 1087   | 5 Q25961  | Q25961 plasmodium   |

|    |      |      |      |           |                    |
|----|------|------|------|-----------|--------------------|
| 17 | 42.5 | 57.4 | 1694 | 5 Q9NHX1  | Q9nhx1 plasmodium  |
| 18 | 42.5 | 57.4 | 1694 | 5 Q9T2T5  | Q9t2t5 plasmodium  |
| 19 | 42.5 | 57.4 | 1704 | 5 Q9T2T4  | Q9t2t4 plasmodium  |
| 20 | 42.5 | 57.4 | 1720 | 5 Q25922  | Q25922 plasmodium  |
| 21 | 42   | 56.8 | 1333 | 5 Q24262  | Q24262 drosophila  |
| 22 | 41.5 | 56.1 | 84   | 13 Q9DEK4 | Q9dek4 coregonus s |
| 23 | 41.5 | 56.1 | 85   | 7 Q95IS3  | Q95is3 salmo salar |
| 24 | 41.5 | 56.1 | 85   | 7 Q95IR2  | Q95ir2 salmo salar |
| 25 | 41.5 | 56.1 | 149  | 7 Q31495  | Q31495 oncorhynch  |
| 26 | 41.5 | 56.1 | 216  | 7 Q9GJH0  | Q9gjh0 salmo trutt |
| 27 | 41.5 | 56.1 | 216  | 7 Q9GJG9  | Q9gig9 salmo trutt |
| 28 | 41   | 55.4 | 247  | 11 Q9D3B9 | Q9d3b9 mus musculu |
| 29 | 41   | 55.4 | 384  | 4 Q9HD07  | Q9hd07 homo sapien |
| 30 | 41   | 55.4 | 447  | 16 Q97HK7 | Q97hk7 clostridium |
| 31 | 41   | 55.4 | 532  | 5 Q96671  | Q96671 drosophila  |
| 32 | 41   | 55.4 | 540  | 5 Q9VU53  | Q9vu53 drosophila  |
| 33 | 40.5 | 54.7 | 67   | 7 Q31577  | Q31577 salmo salar |
| 34 | 40.5 | 54.7 | 67   | 7 Q31581  | Q31581 salmo salar |
| 35 | 40.5 | 54.7 | 67   | 7 Q31582  | Q31582 salmo salar |
| 36 | 40.5 | 54.7 | 71   | 7 Q9XRH1  | Q9xrh1 salvelinus  |
| 37 | 40.5 | 54.7 | 71   | 7 Q9XRH6  | Q9xrh6 salvelinus  |
| 38 | 40.5 | 54.7 | 84   | 13 Q9DEJ6 | Q9dej6 coregonus s |
| 39 | 40.5 | 54.7 | 85   | 7 Q95IS9  | Q95is9 salmo salar |
| 40 | 40.5 | 54.7 | 85   | 7 Q95IS8  | Q95is8 salmo salar |
| 41 | 40.5 | 54.7 | 85   | 7 Q95IS6  | Q95is6 salmo salar |
| 42 | 40.5 | 54.7 | 85   | 7 Q95IS5  | Q95is5 salmo salar |
| 43 | 40.5 | 54.7 | 85   | 7 Q95HY2  | Q95hy2 salmo salar |
| 44 | 40.5 | 54.7 | 85   | 7 Q95HY0  | Q95hy0 salmo salar |
| 45 | 40.5 | 54.7 | 85   | 7 Q95HX9  | Q95hx9 salmo salar |

#### ALIGNMENTS

#### RESULT 1

Q93N27 PRELIMINARY; PRT; 1310 AA.  
ID Q93N27  
AC Q93N27;  
DT 01-DEC-2001 (TREMREL. 19, Created)  
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE TETANUS TOXIN (FRAGMENT).  
OS Clostridium tetani.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shumin Z., Dianliang L.;  
RT "Cloning and sequence analysis of tetanus toxin gene."  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF389424; AAK72964.2;  
FT NON\_TER 1  
FT NON\_TER 1310  
SQ SEQUENCE 1310 AA; 150316 MW; 9EADDC914418E450 CRC64;

Query Match 100.0%; Score 74; DB.2; Length 1310;

Best Local Similarity 100.0%; Pred. No. 0.00014;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15

|||||

Db 831 QYIKANSKFIGITEL 845

#### RESULT 2

Q31585 PRELIMINARY; PRT; 60 AA.  
ID Q31585  
AC Q31585;  
DT 01-NOV-1996 (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE (DB02) MHC CLASS II BETA 1 (FRAGMENT).

```

OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Grimholt U., Olasaker I., de Vries Lindstrom C., Lie O.;
RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
FT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L24953; AAA49597.1;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6776 MW; 5D4F3449060940E2 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 60;
Best Local Similarity 55.6%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 16 EYIRFNSTVGKFGVGYTEL 33

RESULT 3
Q9XRJ9 PRELIMINARY; PRT; 71 AA.
AC Q9XRJ9;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC CLASS II BETA 1 (FRAGMENT).
GN SANA.
OS Salvelinus namaycush (lake trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
OX NCBI_TaxID=8040;
RN [1]
RP SEQUENCE FROM N.A.
RA Dorschner M.O., Duris T., Phillips R.B.;
RT "Diversity of a Lake Trout Mhc class II Gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF130026; AAD20889.1;
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta.1.
DR ProDom; PD000328; MHC_II_beta.1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1
FT NON_TER 71
SQ SEQUENCE 71 AA; 8002 MW; E3095286582A9F2D CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 71;
Best Local Similarity 55.6%; Pred. No. 1.4;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 14 EYIRFNSTVGKFGVGYTEL 31

RESULT 4
Q95IS2 PRELIMINARY; PRT; 85 AA.
AC Q95IS2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

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DE MHC CLASS II BETA CHAIN (FRAGMENT).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RA Landry C., Bernatchez L.;
RT "Comparative analysis of population structure across environments and
FT geographic scales at Major Histocompatibility Complex and
RL microsatellite in Atlantic salmon (Salmo salar).";
DR Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF373699; AAK61882.1;
KW MHC.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9743 MW; 3214E01AD1B66AC5 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 85;
Best Local Similarity 55.6%; Pred. No. 1.7;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 33 EYIRFNSTVGKFGVGYTEL 50

RESULT 5
Q95HY1 PRELIMINARY; PRT; 85 AA.
AC Q95HY1;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
GN DBI.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21383619; PubMed-11491536;
RA Langefors A., Lohm J., von Schantz T.;
RT "Allelic polymorphism in MHC class II B in four populations of
FT Atlantic salmon (Salmo salar).";
RL Immunogenetics 53:329-336(2001).
DR EMBL; AF104370; AAL04002.1;
KW MHC.
FT NON_TER 1
FT NON_TER 85
SQ SEQUENCE 85 AA; 9723 MW; 27C9F7931F1F01C4 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 85;
Best Local Similarity 55.6%; Pred. No. 1.7;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

Qy 1 QYIKANS---KFIGITEL 15
Db 33 EYIRFNSTVGKFGVGYTEL 50

RESULT 6
Q95HX4 PRELIMINARY; PRT; 86 AA.
AC Q95HX4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MHC CLASS II B ANTIGEN (FRAGMENT).
GN DBI.

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OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383619; PubMed=11491536;
RA Langefors A., Lohm J., von Schantz T.;
RT "Allelic polymorphism in MHC class II B in four populations of
RT Atlantic salmon (Salmo salar).";
RL Immunogenetics 53:329-336(2001).
DR EMBL; AF104377; AAL04009.1; -.
KW MHC.
FT NON_TER 1 86
FT NON_TER 86 86
SQ SEQUENCE 86 AA; 9312 MW; E5097729F681F149 CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 86;
Best Local Similarity 55.6%; Pred. No. 1.7;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 33 EYIRFNSVGVKFGVGYTEL 50

RESULT 7
Q31590
ID Q31590 PRELIMINARY; PRT; 244 AA.
AC Q31590;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC CLASS II.
GN MHC-SASA CLASS II B.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93170890; PubMed=8436418;
RA Hordvik I., Grimholt U., Fosse V.M., Lie Y., Endresen C.;
RT "Cloning and sequence analysis of cDNAs encoding the MHC class II a-
RT chain in Atlantic salmon, Salmo salar.";
RL Immunogenetics 37:437-441(1993).
DR EMBL; X70166; CAA49725.1; -.
DR HSP; P01888; IIMG.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
DR SMART; SM00407; Igcl; 1.
KW Glycoprotein; MHC II; Transmembrane.
SQ SEQUENCE 244 AA; 27449 MW; 496CB9EA9D73765C CRC64;

Query Match 60.1%; Score 44.5; DB 7; Length 244;
Best Local Similarity 55.6%; Pred. No. 5.1;
Matches 10; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 51 EYIRFNSVGVKFGVGYTEL 68

RESULT 8
Q31578
ID Q31578 PRELIMINARY; PRT; 546 AA.
AC Q31578;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE (DB03) MHC CLASS II BETA 1 (FRAGMENT).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
RT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L24929; AAA49590.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 67
FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7449 MW; 42771AEDBABA6626 CRC64;

Query Match 58.8%; Score 43.5; DB 7; Length 67;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 16 EYIRFNSVGVKFGVGYTEL 33

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AC Q9XG37;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 66.2 KDA PROTEIN.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087226; PubMed=10618395;
RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
RA Cavalier-Smith T., Maier U., Douglas S.;
RT "Chloroplast protein and centrosomal genes, a tRNA intron, and odd
RT telomeres in an unusually compact eukaryotic genome, the cryptomonad
RT nucleomorph.";
RL Nature 410:1091-1096(2001).
DR EMBL; AJ010592; CAB40403.1; -.
KW Hypothetical protein.
SQ SEQUENCE 546 AA; 66218 MW; 7303950F632BE6F2 CRC64;

Query Match 59.5%; Score 44; DB 10; Length 546;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 YIKANSKFIGITEL 15
   :||: ||: ||: ||:
Db 445 FIKNSRFRMLTEI 458

RESULT 9
Q31578
ID Q31578 PRELIMINARY; PRT; 67 AA.
AC Q31578;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE (DB03) MHC CLASS II BETA 1 (FRAGMENT).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;
RT "A study of polymorphism in the MHC class II beta 1 and MHC class I
RT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L24929; AAA49590.1; -.
DR InterPro; IPR000353; MHC_II_beta.
DR Pfam; PF00969; MHC_II_beta; 1.
DR ProDom; PD000328; MHC_II_beta; 1.
KW Glycoprotein; MHC II; Transmembrane.
FT NON_TER 1 67
FT NON_TER 67 67
SQ SEQUENCE 67 AA; 7449 MW; 42771AEDBABA6626 CRC64;

Query Match 58.8%; Score 43.5; DB 7; Length 67;
Best Local Similarity 50.0%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 1 OYIKANS---KFIGITEL 15
   :||: || ||: |||
Db 16 EYIRFNSVGVKFGVGYTEL 33

```

## RESULT 10

Q9CF66 PRELIMINARY; PRT; 180 AA.  
 AC Q9CF66; 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE SPERMIDINE ACETYLTRANSFERASE (EC 2.3.1.57).  
 GN YOFF.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Lactococcus.  
 OX NCBI\_TaxID=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=IL1403;  
 RX MEDLINE=21235186; PubMed=11337471;  
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
 lactis ssp. lactis IL1403.";  
 LA ENBL; AE006391; AAK05713.1;  
 DR InterPro; IPR000182; Acetyltransf\_GCN5.  
 DR Pfam; PF00583; Acetyltransf; 1.  
 KW Transferase; Complete proteome.  
 SQ SEQUENCE 180 AA; 21022 MW; 6DBD148524C0DF3C CRC64;

Query Match 58.1%; Score 43; DB 16; Length 180;  
 Best Local Similarity 69.2%; Pred. No. 6.9;  
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

## QY 3 IKANSKFIGITEL 15

I:|||||  
 65 IEANDTFIGIVEL 77

## RESULT 11

Q9MCL7 PRELIMINARY; PRT; 250 AA.  
 AC Q9MCL7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE ORF13.  
 GN ORF13.  
 OS Streptococcus thermophilus bacteriophage 7201.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
 OX NCBI\_TaxID=112023;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20088830; PubMed=10620678;  
 RA Stanley E., Walsh L., van der Zwet A., Fitzgerald G.F.,  
 RA van Sinderen D.;  
 RT "Identification of four loci isolated from two Streptococcus  
 thermophilus phage genomes responsible for mediating bacteriophage  
 resistance.";  
 RT FEMS Microbiol. Lett. 182:271-277(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Stanley E., Walsh L., Fitzgerald G.F., van Sinderen D.;  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF145054; AAF43506.1;  
 DR InterPro; IPR002295; D21N6\_mtfase.  
 DR InterPro; IPR001091; N4\_Mtase.  
 DR Pfam; PF01555; N6\_N4\_Mtase.  
 DR PRINTS; PR00506; D21N6MTFRASE.  
 DR PRINTS; PR00508; S21N4MTFRASE.  
 SQ SEQUENCE 250 AA; 28744 MW; 725EA3B2B56B0D7F CRC64;

Query Match 58.1%; Score 43; DB 9; Length 250;

Best Local Similarity 57.1%; Pred. No. 9.7;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

## QY 1 QYIKANSKFIGITE 14

I:|||||  
 131 QVLKANKKIVGATE 144

## RESULT 12

Q9XJE8 PRELIMINARY; PRT; 252 AA.  
 AC Q9XJE8;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PUTATIVE METHYLASE.  
 OS Lactococcus lactis bacteriophage Tuc2009.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
 OX NCBI\_TaxID=35241;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Sinderen D., van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F.;  
 RT "Molecular analysis of the temperate lactococcal phage Tuc2009.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF109874; AAD37103.1;  
 DR InterPro; IPR002295; D21N6\_mtfase.  
 DR InterPro; IPR001091; N4\_Mtase.  
 DR InterPro; IPR002941; N6\_N4\_Mtase.  
 DR Pfam; PF01555; N6\_N4\_Mtase; 1.  
 DR PRINTS; PR00506; D21N6MTFRASE.  
 DR PRINTS; PR00508; S21N4MTFRASE.  
 KW Methyltransferase.  
 SQ SEQUENCE 252 AA; 29357 MW; 4D5A59FF47363948 CRC64;

Query Match 58.1%; Score 43; DB 9; Length 252;

Best Local Similarity 57.1%; Pred. No. 9.8;  
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

## QY 1 QYIKANSKFIGITE 14

I:|||||  
 130 QVLKANKKIVGATE 143

## RESULT 13

Q9CRV4 PRELIMINARY; PRT; 302 AA.  
 AC Q9CRV4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 3110030A04RIK PROTEIN (FRAGMENT).  
 GN 3110030A04RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRIONIC HEAD;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Barsh G.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

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RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK014093; BAB29151.1; -
DR HSP: Q02410; 1AQC
DR MGD: MGI:1920407; j110030A04Rik.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000050; PID_domain.
DR Pfam: PF00640; PID; 1.
DR SMART: SM00462; PTB; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR PROSITE: PS01179; PID; 1.
FT NON_TER 1
SEQUENCE 302 AA; 34207 MW; 8CB11440F898C65A CRC64;
Query Match 58.1%; Score 43; DB 11; Length 302;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 YIKANSKFIGITEL 15
DB 22 YIPYNAKFLGSTE 35
II I:II:II:
RESULT 14
ID Q9CYD2 PRELIMINARY; PRT; 309 AA.
AC Q9CYD2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 5730529006RIK PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRIO;
RX MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyushaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK017798; BAB30939.1; -
DR HSP: Q02410; 1AQC
DR MGD: MGI:1917926; 5730529006RIK.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR InterPro: IPR000050; PID_domain.
DR Pfam: PF00640; PID; 1.
DR SMART: SM00462; PTB; 1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
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DR PROSITE: PS01179; PID; 1.
SQ SEQUENCE 309 AA; 35272 MW; 535DD8E733C0F406 CRC64;
Query Match 58.1%; Score 43; DB 11; Length 309;
Best Local Similarity 57.1%; Pred. No. 12;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 YIKANSKFIGITEL 15
DB 24 YIPYNAKFLGSTE 37
II I:II:II:
RESULT 15
ID Q9YTK4 PRELIMINARY; PRT; 899 AA.
AC Q9YTK4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF 63.
OS Ateline herpesvirus 3.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=85618;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=73;
RX MEDLINE=20091363; PubMed=10623770;
RA Albrecht J.C.;
RT "Primary structure of the Herpesvirus Ateles genome.";
RL J. Virol. 74:1033-1037(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=73;
RX Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF083424; AAC95587.1; -
SQ SEQUENCE 899 AA; 103389 MW; 19440A7944DE2531 CRC64;
Query Match 58.1%; Score 43; DB 12; Length 899;
Best Local Similarity 64.3%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 OYIKANSKFIGITE 14
DB 124 OYITNSNFTGQPE 137
II I:II:II:II:II:II:
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Job time : 6.83434 secs
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OM protein - protein search, using sw model

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(without alignments)  
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Title: US-09-787-126-34  
Perfect score: 74  
Sequence: 1 QYKANSKFIGITEL 15

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arched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
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2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
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| 1          | 74    | 100.0       | 15     | 2  | US-08-319-704-10  |
| 2          | 74    | 100.0       | 15     | 2  | US-08-661-052-6   |
| 3          | 74    | 100.0       | 15     | 2  | US-08-460-502-7   |
| 4          | 74    | 100.0       | 15     | 4  | US-09-046-373-2   |
| 5          | 74    | 100.0       | 15     | 4  | US-09-188-082-6   |
| 6          | 74    | 100.0       | 15     | 5  | PCT-US93-11703-69 |
| 7          | 74    | 100.0       | 16     | 4  | US-09-248-588-55  |
| 8          | 74    | 100.0       | 17     | 1  | US-08-446-692-4   |
| 9          | 74    | 100.0       | 17     | 2  | US-08-488-351A-4  |
| 10         | 74    | 100.0       | 17     | 3  | US-09-100-409A-40 |
| 11         | 74    | 100.0       | 17     | 5  | PCT-US95-08596-23 |
| 12         | 74    | 100.0       | 17     | 5  | PCT-US95-13841-7  |
| 13         | 74    | 100.0       | 27     | 1  | US-08-446-692-13  |
| 14         | 74    | 100.0       | 27     | 2  | US-08-488-351A-13 |
| 15         | 74    | 100.0       | 31     | 5  | PCT-US93-11703-63 |
| 16         | 74    | 100.0       | 37     | 1  | US-08-446-692-57  |
| 17         | 74    | 100.0       | 37     | 2  | US-08-446-692-63  |
| 18         | 74    | 100.0       | 37     | 2  | US-08-488-351A-57 |
| 19         | 74    | 100.0       | 37     | 2  | US-08-488-351A-63 |
| 20         | 74    | 100.0       | 47     | 1  | US-08-446-692-35  |
| 21         | 74    | 100.0       | 47     | 2  | US-08-488-351A-35 |
| 22         | 70    | 94.6        | 14     | 1  | US-08-186-266-5   |
| 23         | 70    | 94.6        | 14     | 1  | US-08-305-871A-5  |
| 24         | 70    | 94.6        | 14     | 1  | US-08-465-167A-18 |
| 25         | 70    | 94.6        | 14     | 2  | US-08-817-933A-9  |
| 26         | 70    | 94.6        | 14     | 5  | PCT-US92-07218-15 |
| 27         | 70    | 94.6        | 14     | 5  | PCT-US92-07218-30 |

|    |    |      |    |   |                    |                    |
|----|----|------|----|---|--------------------|--------------------|
| 28 | 70 | 94.6 | 14 | 5 | PCT-US95-02121-95  | Sequence 95, Appl  |
| 29 | 70 | 94.6 | 24 | 5 | PCT-US92-07218-25  | Sequence 25, Appl  |
| 30 | 70 | 94.6 | 24 | 5 | PCT-US92-07218-31  | Sequence 31, Appl  |
| 31 | 70 | 94.6 | 24 | 5 | PCT-US95-02121-110 | Sequence 110, Appl |
| 32 | 70 | 94.6 | 27 | 5 | PCT-US92-07218-26  | Sequence 26, Appl  |
| 33 | 70 | 94.6 | 27 | 5 | PCT-US92-07218-27  | Sequence 27, Appl  |
| 34 | 70 | 94.6 | 27 | 5 | PCT-US92-07218-28  | Sequence 28, Appl  |
| 35 | 70 | 94.6 | 27 | 5 | PCT-US92-07218-32  | Sequence 32, Appl  |
| 36 | 70 | 94.6 | 27 | 5 | PCT-US95-02121-111 | Sequence 111, Appl |
| 37 | 70 | 94.6 | 27 | 5 | PCT-US95-02121-112 | Sequence 112, Appl |
| 38 | 70 | 94.6 | 29 | 3 | US-09-075-257A-13  | Sequence 13, Appl  |
| 39 | 70 | 94.6 | 29 | 3 | US-09-075-257A-14  | Sequence 14, Appl  |
| 40 | 70 | 94.6 | 29 | 4 | US-09-534-639-13   | Sequence 13, Appl  |
| 41 | 70 | 94.6 | 29 | 4 | US-09-534-639-14   | Sequence 14, Appl  |
| 42 | 70 | 94.6 | 30 | 5 | PCT-US92-07218-29  | Sequence 29, Appl  |
| 43 | 70 | 94.6 | 32 | 1 | US-08-186-266-9    | Sequence 9, Appl   |
| 44 | 70 | 94.6 | 50 | 4 | US-09-171-969-7    | Sequence 7, Appl   |
| 45 | 69 | 93.2 | 15 | 2 | US-08-661-052-9    | Sequence 9, Appl   |

## ALIGNMENTS

RESULT 1  
US-08-319-704-10  
; Sequence 10, Application US/08319704  
; Patent No. 5814617  
; GENERAL INFORMATION:  
; APPLICANT: Hoffman, Stephen L.  
; APPLICANT: Charoenvit, Yupin  
; APPLICANT: Hedstrom, Richard C.  
; APPLICANT: Doolan, Denise L.  
; TITLE OF INVENTION: Protective 17 kDa Malaria Hepatic and  
; TITLE OF INVENTION: Erythrocytic Stage Immunogen and Gene  
; NUMBER OF SEQUENCE: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Naval Medical R & D Command  
; STREET: Bldg 1, T-12, 8901 Wisconsin Avenue  
; CITY: Bethesda  
; STATE: Maryland  
; COUNTRY: U.S.A  
; ZIP: 20889-5606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/319,704  
; FILING DATE: 07-OCT-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. David Spevack  
; REGISTRATION NUMBER: 24,743  
; REFERENCE/DOCKET NUMBER: 75,206  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 295-6759  
; TELEFAX: (301) 295-1022  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-319-704-10

Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
QY 1 QYKANSKFIGITEL 15  
DB 1 QYKANSKFIGITEL 15

RESULT 2  
US-08-661-052-6  
; Sequence 6, Application US/08661052  
; Patent No. 5837243  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano  
; APPLICANT: Chezian Somsundaram  
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD  
; TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, Suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/661,052  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/484,172  
; FILING DATE: 07-JUNE-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MX1-043CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FRAGMENT TYPE: internal  
; US-08-661-052-6  
Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 QYIKANSKFIGITEL 15  
RESULT 3  
US-08-460-502-7  
; Sequence 7, Application US/08460502  
; Patent No. 5843464  
; GENERAL INFORMATION:  
; APPLICANT: Bakaletz, Lauren O.  
; APPLICANT: Kawaya, Parvin T.  
; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides  
; NUMBER OF SEQUENCES: 11.  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Calfee, Halter and Griswold  
; STREET: 800 Superior Avenue  
; CITY: Cleveland  
; STATE: Ohio  
; COUNTRY: U.S.A.  
; ZIP: 44114-2688  
Query Match 100.0%; Score 74; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 QYIKANSKFIGITEL 15  
RESULT 4  
US-09-046-373-2  
; Sequence 2, Application US/09046373  
; Patent No. 6235714  
; GENERAL INFORMATION:  
; APPLICANT: Sudhir Paul  
; APPLICANT: Larry J. Smith  
; APPLICANT: Gennady Gololobov  
; TITLE OF INVENTION: Methods for Identifying Inducers and  
; TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: UNMC 63123  
; CURRENT APPLICATION NUMBER: US/09/046,373  
; CURRENT FILING DATE: 1998-03-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Clostridium tetani  
; US-09-046-373-2  
Query Match 100.0%; Score 74; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 5  
US-09-188-082-6  
; Sequence 6, Application US/09188082  
; Patent No. 6270765  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,502  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Golrick, Mary E.  
; REGISTRATION NUMBER: 34,829  
; REFERENCE/DOCKET NUMBER: 22727/00120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (216) 622-8458  
; TELEFAX: (216) 241-0816  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-460-502-7  
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Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
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Db 1 QYIKANSKFIGITEL 15  
RESULT 4  
US-09-046-373-2  
; Sequence 2, Application US/09046373  
; Patent No. 6235714  
; GENERAL INFORMATION:  
; APPLICANT: Sudhir Paul  
; APPLICANT: Larry J. Smith  
; APPLICANT: Gennady Gololobov  
; TITLE OF INVENTION: Methods for Identifying Inducers and  
; TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their  
; TITLE OF INVENTION: Use  
; FILE REFERENCE: UNMC 63123  
; CURRENT APPLICATION NUMBER: US/09/046,373  
; CURRENT FILING DATE: 1998-03-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Clostridium tetani  
; US-09-046-373-2  
Query Match 100.0%; Score 74; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
Db 1 QYIKANSKFIGITEL 15  
RESULT 5  
US-09-188-082-6  
; Sequence 6, Application US/09188082  
; Patent No. 6270765  
; GENERAL INFORMATION:  
; APPLICANT: Yashwant M. Deo  
; APPLICANT: Joel Goldstein  
; APPLICANT: Robert Graziano

APPLICANT: Chezian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-PC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: Internal  
US-09-188-082-6  
Query Match 100.0%; Score 74; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
RESULT 6  
PCT-US93-11703-69  
Sequence 69, Application PC/TUS9311703  
GENERAL INFORMATION:  
APPLICANT: Chiron Mimotopes Pty. Ltd.  
TITLE OF INVENTION: T-Cell Epitopes  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grant D. Green  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11703  
FILING DATE: 28-DEC-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/984,852  
FILING DATE: 02-DEC-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D.  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0222.101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2706  
TELEFAX: 510-655-3542  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-11703-69  
Query Match 100.0%; Score 74; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.3e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
RESULT 7  
US-09-248-588-55  
Sequence 55, Application US/09248588  
Patent No. 6231864  
GENERAL INFORMATION:  
APPLICANT: Birkett, Ashley J.  
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and  
their Derivatives  
FILE REFERENCE: SYN-101 4564/69529  
CURRENT APPLICATION NUMBER: US/09/248,588  
CURRENT FILING DATE: 1999-02-11  
EARLIER FILING DATE: 1998-02-12  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 55  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Clostridium tetani  
PUBLICATION INFORMATION:  
JOURNAL: Vaccine  
VOLUME: 15  
ISSUE: 4  
PAGES: 377-  
DATE: 1997  
US-09-248-588-55  
Query Match 100.0%; Score 74; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QYIKANSKFIGITEL 15  
DB 1 QYIKANSKFIGITEL 15  
RESULT 8  
US-08-446-692-4  
Sequence 4, Application US/08446692  
Patent No. 5759551  
GENERAL INFORMATION:  
APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
and synthetic universal immune stimulators for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-4

Query Match 100.0%; Score 74; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIGITEL 15
Db 3 QYKANSKFIGITEL 17

RESULT 9
US-08-488-351A-4
; Sequence 4, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994

; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,409A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-409A-40

Query Match 100.0%; Score 74; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIGITEL 15
Db 3 QYKANSKFIGITEL 17

RESULT 10
US-09-100-409A-40
; Sequence 40, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
; TITLE OF INVENTION: IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,409A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 1151-4154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-100-409A-40

Query Match 100.0%; Score 74; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIGITEL 15
Db 3 QYKANSKFIGITEL 17
```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYKANSKFIGITEL 15  
Db 3 QYKANSKFIGITEL 17

## RESULT 11

PCT-US95-08596-23  
; Sequence 23, Application PC/TUS9508596

## ; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Proinsulin Peptide Compounds for Detecting

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08596

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/272,220

; FILING DATE: 08-JULY-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A., Jr.

; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: DCI-092PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)227-5941

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

PCT-US95-08596-23

Query Match 100.0%; Score 74; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYKANSKFIGITEL 15  
Db 3 QYKANSKFIGITEL 17

## RESULT 12

PCT-US95-13841-7

; Sequence 7, Application PC/TUS9513841

## ; GENERAL INFORMATION:

; APPLICANT: United Biomedical Inc; Walfield, Alan M.;

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: Synthetic Ige Membrane Anchor

; TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy

; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Maria C.H. Lin

; STREET: 345 Park Avenue

; CITY: New York

STATE: NY  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13841  
FILING DATE: 25-OCT-1995

## CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/328,519

FILING DATE: 25-OCT-1994

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lin, Maria C.H.

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4117

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-758-4800

TELEFAX: 212-751-6849

TELEX: 421792

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US95-13841-7

Query Match 100.0%; Score 74; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.5e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QYKANSKFIGITEL 15  
Db 3 QYKANSKFIGITEL 17

## RESULT 13

US-08-446-692-13

; Sequence 13, Application US/08446692

; Patent No. 5759551

## ; GENERAL INFORMATION:

; APPLICANT: Ladd, Anna

; APPLICANT: Wang, Chang Yi

; APPLICANT: Zamb, Timothy

; TITLE OF INVENTION: Immunogenic LHRH peptide constructs

; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

; NUMBER OF SEQUENCES: 114

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Maria C.H. Lin

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10154-0053

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,692

; FILING DATE: 7-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Maria C.H. Lin

; REGISTRATION NUMBER: 29,323

; REFERENCE/DOCKET NUMBER: 1151-4146 US2

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-446-692-13

Query Match 100.0%; Score 74; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYIKANSKFIGITEL 15  
DB 3 QYIKANSKFIGITEL 17

RESULT 14  
US-08-488-351A-13  
Sequence 13, Application US/08488351A  
Patent No. 5843446  
GENERAL INFORMATION:

APPLICANT: Ladd, Anna  
APPLICANT: Wang, Chang Yi  
APPLICANT: Zamb, Timothy  
TITLE OF INVENTION: Immunogenic LHRH peptide constructs  
TITLE OF INVENTION: and synthetic universal immune stimulants for vaccines  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin  
STREET: 345 Park Avenue  
CITY: New York  
STATE: NY  
COUNTRY: US

ZIP: 10154-0053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,351A  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/446,692  
FILING DATE: 7-JUN-1995  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/229,275  
FILING DATE: 14-APR-1994  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,166  
FILING DATE: 27-APR-1992  
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Maria C.H. Lin  
REGISTRATION NUMBER: 29,323  
REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)415-8745  
TELEFAX: (516)751-6849

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 27 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-488-351A-13

Query Match 100.0%; Score 74; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYIKANSKFIGITEL 15  
DB 3 QYIKANSKFIGITEL 17

RESULT 15  
PCT-US93-11703-63  
Sequence 63, Application PC/TUS9311703  
GENERAL INFORMATION:

APPLICANT: Chiron Mimotopes Pty. Ltd.  
TITLE OF INVENTION: T-Cell Epitopes  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Grant D. Green  
STREET: 4560 Horton St.  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.308  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/11703  
FILING DATE: 28-DEC-1993  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/984,852  
FILING DATE: 02-DEC-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Green, Grant D.  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 0222.101

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 510-601-2706  
TELEFAX: 510-655-3542

INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 31 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-11703-63

Query Match 100.0%; Score 74; DB 5; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QYIKANSKFIGITEL 15  
DB 10 QYIKANSKFIGITEL 24

Search completed: October 10, 2002, 16:03:56  
Job time: 2.80723 secs